

SEQUENCE CHARACTERISTICS:
LENGTH: 149 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 385234
US-08-963-409-3

Alignment Scores:
Pred. No.: 5,12e-10 Length: 149
Score: 159.00 Matches: 44
Percent Similarity: 50.00% Conservative: 39
Best Local Similarity: 26.51% Mismatches: 55
Query Match: 14.99% Indels: 28
DB: 3 Gaps: 6

US-10-021-323-13 (1-609) x US-08-963-409-3 (1-149)

QY 550 AAAATGCCCCCTTAGTAAGACCGACTTGCAACGGCTATTGCGAAGCTGCACAGAAAT 491
DB 4 LysleuThrGluGluGlnIleSerGluPheLysGluAlaPheSerLeuPheAsp 23
QY 490 GGAGATGGCTTGTAGTCTGAGAGAGCTGAATTGGTCTCCAGAGATCCGG----- 437
DB 24 GlyAspGlyThrIleThrThrIleGluLeuGlyThrValMetArgSerLeuGlyGln 43
QY 436 -----TCTGTCCAATTACCTTGAAGAAATGGAGCCCTTGAAGTGGAAACCA 389
DB 44 ProThrGluAlaGluLeuGlnAspMetIleAsnGluIleAsp---ThrAspGlyAsnGly 62
QY 388 TGTTCGACCTTGATGAAATCTTGTCTTTATGATCATCTGCAGACCCACTGCACAT 329
DB 63 ThrIleAspPheProGluPheLeuThrIle-----MetAlaArgLysLeuLys--- 78
QY 328 GGTGTGTACGAGAGAGAGAGAGAGATGTGATTCATTCACGGCGCGGTGAAGAGAGAC 269
DB 79 -----AspThrAspThrGluGluGluLeuIle----- 87
QY 268 AGTGACCTTGCAGAGCTTTTAAAGTGTTCGACTTGATGGGATGGGAGGATGT 209
DB 88 -----GluAlaPheArgValPheAspArgAspGlyAspGlyTyrIleSerAla 103
QY 208 GAGAGCTTGATGAGTGTGCTGGAGAGACTGGTATGTAGCGAAATAGTGAAAGAC 149
DB 104 AspGluLeuArgHisValMetThrAsnLeuGly-----GluLysLeuThrAsnGluGlu 121
QY 148 TGCAGAGCATGATTTGTATTACGACACCAATTCAGACGGCATGTTGATTTTCAGAA 89
DB 122 ValAspGluMetIleArgGluAlaAspIleAspGlyAspGlyGlnIleAsnTyrGluGlu 141
QY 88 TTCAAAAACATGATGTTA 71
DB 142 PheValLysMetMetIle 147

RESULT 2

US-09-239-909-2
Sequence 2, Application US/09239909
Patent No. 6284952
GENERAL INFORMATION:
APPLICANT: Kumbo Petrochemical Co. Ltd.
TITLE OF INVENTION: Transgenic Plants with Divergent SCAM4 or SCAM5 Gene to Achieve N
FILE REFERENCE: P99-2-6
CURRENT APPLICATION NUMBER: US/09/239,909
EARLIER FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: EP 99300136.1
NUMBER OF SEQ ID NOS: 4
SOFTWARE: KODATIN 1.0
SEQ ID NO 2
LENGTH: 150
TYPE: PRT

ORGANISM: G. max calmodulin4 (SCAM4)
US-09-239-909-2

Alignment Scores:
Pred. No.: 1.5e-09 Length: 150
Score: 155.00 Matches: 47
Percent Similarity: 47.20% Conservative: 29
Best Local Similarity: 29.19% Mismatches: 57
Query Match: 14.61% Indels: 28
DB: 3 Gaps: 5

US-10-021-323-13 (1-609) x US-09-239-909-2 (1-150)

QY 526 GACTTGCAACCGCTGATTCGAGAAAGCTGCACAGAGATGAGTGGCTTCGTAGTCTGAG 467
DB 12 AspPheLysGluAlaPheGlyLeuPheAspLysAspGlyAspGlyCysIleThrValGlu 31
QY 466 GAGCTGAATTGGTGTCTCCAGAGATCGGCTGTCTCAATTACGCTTGAAGAAATGAG 407
DB 32 GluLeuAlaThrValIleArgSerLeuAspGln---AsnProThrGluGluGluLeuGln 50
QY 406 CCCTTAGT-----GAAAACCATGTTGAACCTTGATGATTTCTTG 365
DB 51 AspMetIleSerGluValAspAlaAspGlyAsnGlyThrIleGluPheAspGluPheLeu 70
QY 364 TTCTTTATGATTCATCTCGAACCCACTGCACATGCTGTGTGACGAAAGAGAGAGAG 305
DB 71 -----SerLeuMetAlaLysValLysValLysAspThrAspAlaGluGluGlu--- 85
QY 304 GAATGTGTCATTCACGGCGCGGTGAAGAGACAGTGCCTTGCAGAGCTTTTAA 245
DB 86 -----LeuLysGluAlaPheLys 91
QY 244 GTGTTGACTTGATGGGAGATGGTGGGAGATGAGAGCTTGAAATAGTCTGGGA 185
DB 92 ValPheAspLysAspGlnAsnGlyTyrIleSerAlaSerGluLeuArgHisValMetIle 111
QY 184 AGACTGGTATGATGAGTGAATAATGAGTGAAGACTGCAGACATGATTTGTAATTAC 125
DB 112 AsnLeuGly-----GluLysLeuThrAspGluIleValGluGlnMetIleLysGluAla 129
QY 124 GACCAATTCAGACGGCATGTTGATTTTCAGAAATTCAAAAACATGATTTACATTC 65
DB 130 AspLeuAspGlyAspGlyGlnValAsnTyrGluGluPheValLysMetMetThrVal 149
QY 64 CGT 62
DB 150 Arg 150

RESULT 3

US-08-602-941-1
Sequence 1, Application US/08602941
Patent No. 5837680
GENERAL INFORMATION:
APPLICANT: Moses, Marsha A.
APPLICANT: Langer, Robert S.
APPLICANT: Wiedersheim, Dimitri G.
APPLICANT: Wu, Immin
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS
TITLE OF INVENTION: COMPRISING TROPONIN SUBUNITS, FRAGMENTS AND ANALOGS
TITLE OF INVENTION: THERMOF AND METHODS OF THEIR USE TO INHIBIT ANGIOGENESIS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible

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1 OPERATING SYSTEM: DOS
2 SOFTWARE: FastSEO version 2.0
3 CURRENT APPLICATION DATA:
4 APPLICATION NUMBER: US/08/602,941
5 FILING DATE: 16-FEB-1996
6 CLASSIFICATION: 514
7 ATTORNEY/AGENT INFORMATION:
8 NAME: Poissant, Brian M.
9 REGISTRATION NUMBER: 28,452
10 REFERENCE/DOCKET NUMBER: 8657-021-999
11 TELECOMMUNICATION INFORMATION:
12 TELEPHONE: 212-790-9090
13 TELEFAX: 212-869-8864/9741
14 INFORMATION FOR SEQ ID NO: 1:
15 SEQUENCE CHARACTERISTICS:
16 LENGTH: 160 amino acids
17 TYPE: amino acid
18 STRANDEDNESS: single
19 TOPOLOGY: linear
20 MOLECULE TYPE: No. 5837680e
21 FEATURE:
22 NAME/KEY: Peptide
23 LOCATION: 1..160
24 OTHER INFORMATION:
25 OTHER INFORMATION: Muscle troponin C
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Alignment Scores:
Pred. No.:          3e-09      Length:      160
Score:             15.5      Matches:     43
Percent Similarity: 45.86%    Mismatches: 29
Best Local Similarity: 27.39% Conservative: 60
Query Match:       14.37%    Indels:      0
DB:                2        Gaps:        4

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US-10-021-323-13 (1-609) x US-08-602-941-1 (1-160)

[illegible]

RESULT 4
US-08-961-264-1
; Sequence 1, Application US/08961264
; Patent No. 6025331

GENERAL INFORMATION:
APPLICANT: Moses, Marsha A.
APPLICANT: Langer, Robert S.
APPLICANT: Wiederschain, Dimitri G.
APPLICANT: Wu, Immin
APPLICANT: Sytkowski, Arthur
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS
TITLE OF INVENTION: COMPOSITING TROPONIN SUBUNITS, FRAGMENTS AND ANALOGS
TITLE OF INVENTION: THEREOF AND METHODS OF THEIR USE TO INHIBIT ANGIOGENESIS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,264
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,941
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,452
REFERENCE/DOCKET NUMBER: 8657-021-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864/9741
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 160 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6025331e
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..160
OTHER INFORMATION: /label= Human Fast Twitch Skeletal
OTHER INFORMATION: Muscle Troponin C
US-08-961-264-1

Alignment Scores:	
Pred. No.:	3e-09
Score:	152.50
Percent Similarity:	45.88%
Best Local Similarity:	27.39%
Query Match:	14.37%
DB:	3
	Gaps:

[illegible]

Db	78	ValMetMetValArgGlnMetLysbLysAspAlaLysGlybSerGluGluGlu-----	95
Oy	304	GAATTGGTCATTCCACGGCGCGCGTGAAGAAGAAGACAGTGCATCTTGGCAAGCTTTTAA	245
Ab	96	-----LeuAlaGluLysPheArg	101
Oy	244	GTGTTGACTTGAATGGAGATGGCGTTGGCGGCGATGTGAGAGCTTGAATACGTCGTGGA	185
Db	102	ILepheAPbAPASAspAlaAspGlyLysLysPheArgGluGluLeuAlaGluLLePheArg	121
Oy	184	AGACGTGGTATGTGTAGGTGAAAAATGTGTGAAAGACATCAGACAGCATGATTGGATATAC	125
Db	122	AlaSerGly-----GluHisValAlaThrAspGluGluLLeGluSerLeuMetLysAspGly	139
Oy	124	GACACCAATTCAAGACGCGATGGTGAATTTTCAAGATTTCAAAAACATGATG	74
Db	140	AspLysAsnAsnAspGlyLysArgLLeAspPheAspGluPheLysbLysMetMet	156

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RESULT 5
US-09-442-099A-1
; Sequence 1, Application US/09442099A
; Patent No. 6465431
; GENERAL INFORMATION:
; APPLICANT: Thorm, R.
; APPLICANT: Lansen, M.
; APPLICANT: Moses, M.
; APPLICANT: Wieserschain, D.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS COMPRISING TROPONIN SUBUNITS,
; TITLE OF INVENTION: FRAGMENTS AND HOMOLOGS THEREOF AND METHODS OF THEIR USE
; TITLE OF INVENTION: INHIBIT ANGIOGENESIS
; FILE REFERENCE: 8657-028
; CURRENT APPLICATION NUMBER: US/09/442,099A
; CURRENT FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: 09/268,274
; PRIOR FILING DATE: 1999-03-15
; PRIOR APPLICATION NUMBER: 08/961,264
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: 08/602,941
; PRIOR FILING DATE: 1996-02-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-442-099A-1

Alignment Scores:
Pred. No.:      3e-09      Length:      160
Score:          152.50     Matches:      43
Percent Similarity: 45.86% Conservative: 29
Best Local Similarity: 27.39% Mismatches: 60
Query Match:     14.37%   Indels:      25
DB:              4        Gaps:        4

US-10-021-323-13 (1-609) x US-09-442-099A-1 (1-160)
QY 526 GACTTGCACCGCTATTTCGAGAGCTGCACAGATGAGATGGCTTCGTTAGCTCGAG 467
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Db 19 Gluhelysblalaalaphaspmechephaspalaapgllygllyaspilsevalyls 38
QY 466 GAGCTGAATGGTGTCTCCAGAGATCGGATCTGTCCAAATTCACCTTGAAAGATTGGAG 407
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Db 39 GluheluglythrValmetArgmetleuglyglnthrPro---ThrlysgluGluleuasp 57
QY 406 CCCTTAGTG-----GGAAAACCATGTTGAACTTGATGATTTCTTG 365
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Db 58 AlalleileglugluvalaspgluaspilyserglyThrilleaspneglugluPhelu 77
QY 364 TTCCTTTATGATCCATCTGCAGACCCACTGCACATGGTGTGTACGAGAGAGAGAGAG 305
   ::||  ::||  ::||  ::||  ::||  ::||  ::||  ::||  ::||  ::||
Db 78 ValmetcevalArglmetlelysgluaspalaelysglylsersgluglu----- 95

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[illegible]

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RESULT 6
US-09-612-342-1
Sequence 1, Application US/09612342
Patent No. 6585401
GENERAL INFORMATION:
APPLICANT: Thorn, R.
APPLICANT: Lanser, M.
APPLICANT: Moses, M.
APPLICANT: Wiederschain, D.
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS COMPRISING
TITLES OF INVENTION: THROPONIN SUBUNITS, FRAGMENTS AND HOMOLOGS THEREOF AND
METHODS OF THEIR USE TO INHIBIT ANGIOGENESIS
FILE REFERENCE: 8657-026
CURRENT APPLICATION NUMBER: US/09/612,342
PRIORITY FILING DATE: 2000-07-06
PRIOR APPLICATION NUMBER: US/09/268,274
PRIOR FILING DATE: 1999-03-15
PRIOR APPLICATION NUMBER: 08/961,264
PRIOR FILING DATE: 1997-10-30
PRIOR APPLICATION NUMBER: 08/602,941
PRIOR FILING DATE: 1996-02-16
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 160
TYPE: PRT
ORGANISM: Homo sapiens
US-09-612-342-1

Alignment Scores:
Pred. No.:      3e-09      Length:      160
Score:          152.50     Matches:      43
Percent Similarity: 45.86%   Conservative: 29
Best Local Similarity: 27.33%  Mismatches: 60
Query Match:    14.37%     Indels:       25
DB:             Gaps:      4

US-10-021-323-13 (1-609) x US-09-612-342-1 (1-160)
QY      526 GACCTGCAACGGGTATTGGAAGAAGTCACAAAGATGAGATGGCTTGACTCTCGAG 467
Db      :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
        19 GlnPheLYsAlaIaLpheAspMetCpheAspAlaAspLygLyglAspIleSerValys 38
QY      466 GAGCTGAATGGTTCTCTCCAGAGATCGGGTCTGTCCAAATTCAGCCCTTGAAGATTGGAG 407
Db      :||| |::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
        39 GluLeuGIyThrValMetArgMetLeuGIyGlnInthrPro---ThrlySGluGluLeuAap 57
QY      406 CCCTTAGTGC-----GGAAAACCATTGTTGAACCTTGATGAATTTCTTG 365
Db      :::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
        58 AlaIleIleGluGluValaAspLysPelySerGIyThrIleAspNheGIyGluPheLeu 77
QY      364 TTCCTTTATGAATTCATCTCGAACCACTGCGATGATGATGATGATGACGAAGAGAGAGAG 305
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        78 ValMetMeValArgGlnMetLeLyGluAspAlaLySGlySerGIyGluGlu----- 95
QY      304 GAATGGTCATTCACGGCGGGGTGAAGACAAGACATGACCTTGCGAAGGCTTTTAA 245

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DB 96 ----- Leu1a1aLucYsPhearg 101
QY 244 GGTGTTGACTTGATGGAGTGGGTTGGGGGATGTGAGAGCTGAATGACGTGCTGGGA 185
DB 102 TLePheAspAlaGlnAlaAspGlyTyrLeaPheProGlnGlnLeu1a1aGlnLeuPhearg 121
QY 184 AGACTGGTATGTGAGTGAATAATGAGAAAAGACTGAGAGCATGATTTGTTATTTAC 125
DB 122 AlaSerGly-----GlnHsValThrAspGlnGlnLeu1a1aGlnLeuMetCysAspGly 139
QY 124 GACACCAATTCAGACGGCATGGTTGTTTCAAGAAATTCAAAACATGATG 74
DB 140 AspLysAsnAsnAspGlyArgLeaPheAspGlnPheLeuLysMetMet 156
RESULT 7
US-09-239-909-4
Sequence 4, Application US/09239909
Patent No. 6284952
GENERAL INFORMATION:
APPLICANT: Kumho Petrochemical Co. Ltd.
TITLE OF INVENTION: Transgenic Plants with Divergent SCAM4 or SCAM5 Gene to Achieve
FILE REFERENCE: P99-2-6
CURRENT APPLICATION NUMBER: US/09/239,909
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: EP 99300136.1
EARLIER FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 4
SOFTWARE: KOPATIN 1.0
SEQ ID NO 4
LENGTH: 150
TYPE: PRT
ORGANISM: G. max calmodulins (SCAM5)
US-09-239-909-4
Alignment Scores:
Pred. No.: 1,27e-08 Length: 150
Score: 147.00 Matches: 46
Percent Similarity: 49.38% Conservative: 33
Best Local Similarity: 28.75% Mismatches: 51
Query Match: 13.85% Indels: 30
DB: 3 Gaps: 6
US-10-021-323-13 (1-609) x US-09-239-909-4 (1-150)
QY 528 ACCGACTTGCAACGCGTATTCGAGAGCTCGACAGAAATGAGATGGCTTGTACTGTC 470
DB 11 SerGlnLeuLeuGlnAlaPheGlyLeuPheAspLysAspGlyAspGlyCysLeuThrVal 30
QY 469 GAGGAGCTGAATGGTGTCTCCAGAGATCGGGGTCTGTCATTC---AGCCTGAGAGA 413
DB 31 AspGlnPheValThrValLeuArgSerLeu-----ValGlnAsnProThrGlnGlnGln 48
QY 412 TTGAGACCCCTAGTG-----GGAAGAACATGTTGAATTCGATGAA 371
DB 49 LeuGlnAspMetLeuAsnGlnValAspAlaAspGlyAsnGlyThrLeuGlnPheValGln 68
QY 370 TTCTTGTGTTTATTAATCAATCTTCGAACCACTGGCAGATGGTGTGAGAGAGAG 311
DB 69 PheLeu-----AsnLeuMetAlaLysMetLysGlnThrAsp 81
QY 310 GAGGAGGAATGTGCTATTCACGGCGCGGTGAAGAAAGACAGACATGACCTTGCAAGGT 251
DB 82 GlnGlnGln-----AspLeuLysGlnAla 89
QY 250 TTAAAGTGTGACTTGATGAGAGTGGGATGGGTTGGGGGATGAGAGAGCTTGATATCGT 191
DB 90 PheLysValPheAspLysAspGlnAsnGlyTyrLeuSerAlaSerGlnLeuArgHisVal 109
QY 190 CTGGGAGAGCTGGGTATGTGAGGTGAAAATAGTGAAGAAAGACTGACGAGCATGATTTGG 131
DB 110 MetLeuAsnLeuGly-----GlnLysLeuThrAspGlnGlnValGlnGlnMetLeuGln 127

QY 130 TATTACGACACCAATTCAGACGGCATGGTTATTTTCAGAAATTCAAAACATGATGTTA 71
DB 128 GlnAlaAspLeuAspGlyAspGlyGlnValAsnTyrAspGlnPheValLysMetMetMet 147
RESULT 8
US-08-818-253-2
Sequence 2, Application US/08818253
Patent No. 5998204
GENERAL INFORMATION:
APPLICANT: Telen, Roger Y.
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,253
FILING DATE: 14-MAR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07257/043001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5099
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 642 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-818-253-2
Alignment Scores:
Pred. No.: 2.39e-08 Length: 642
Score: 147.00 Matches: 41
Percent Similarity: 50.66% Conservative: 36
Best Local Similarity: 26.97% Mismatches: 57
Query Match: 13.85% Indels: 18
DB: 2 Gaps: 4
US-10-021-323-13 (1-609) x US-08-818-253-2 (1-642)
QY 526 GACTTGCAACGCGTATTCGAGAGCTCGACAGAAATGAGATGGCTTGTACTGAGAG 467
DB 241 GlnPheLysGlnAlaPheSerLeuPheAspLysAspGlyThrLeuThrLys 260
QY 466 GAGCTGAATGGTGTCTCCAGAGATCGGGGTCTGTCATTCAGCTTGA---GAATTTG 410
DB 261 GlnLeuGlyThrValMetArgSerLeuGly-----GlnAsnProThrGlnAlaGlnLeu 278
QY 409 GAGCCCTTAGGGGAAAACATGTTGAATGATGATTCCTGTTTATGATCC 350
DB 279 GlnAspMetLeuAsnGlnValAspAlaAspGlyAsnGlyThrLeuPheProGlnPhe 298
QY 349 ATCTGAAACCACTGACATGTTGTGACGAGAGAGAGAGAGAAATGGTCAATTTCAC 290
DB 299 LeuThrMetMetAlaArgLysMetLysAspThrAspSerGlnGlnGln----- 314

289 GCGGCGGTGAAGAGACAGTGCCTTGGCAAGCTTTAAAGTGTGATTCGAT 230
Db 315 -----IIea:rgluAlaPhearValPheaspIysasp 325
QY 229 GGGGATGGGTGGGGGATGTGAGAGCTTGAATACGTCTGGGAAGACTGGGATGTGA 170
Db 326 GIIAaNglyTYrIlse:raIlaIaGluLeuArGHIsValMetThra:snleugly----- 343
QY 169 GGTGAANAATGAGAAAACACGACGAGCATGATTTGGTATTACGACCAATTCAGAC 110
Db 344 GIuLyLeuThra:spgluValaIaspGluMetIIea:rgluAlaaspIleaspGlyasp 363
QY 109 GGCATGTTGATTTTCAGAAATTCAAAACATGATG 74
Db 364 GIyGlnVala:snTYrGluGluPheValGlnMetMet 375

RESULT 9
US-08-818-252-2
; Sequence 2, Application US/08818252B
; Patent No. 6197928
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Miyawaki, Atsushi
; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
; FILE REFERENCE: 07257/042001
; CURRENT APPLICATION NUMBER: US/08/818,252B
; FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 642
; TYPE: PRP
; ORGANISM: Nequorea victoria
US-08-818-252-2

Alignment Scores:
Pred. No.: 2,39e-08 Length: 642
Score: 147.00 Matches: 41
Percent Similarity: 50.66% Conservative: 36
Best Local Similarity: 26.97% Mismatches: 57
Query Match: 13.85% Indels: 18
Gaps: 4
DB: 3

US-10-021-323-13 (1-609) x US-08-818-252-2 (1-642)

QY 526 GACTTGCAACGCGTATTCGAGAACTCGACAAAGATGAGATGCTTGTAGCTGGAG 467
Db 241 GIuPheLySGluAlaPhe:serLeuPheaspIysaspGlyThriIeThra:Thryls 260
QY 466 GAGCTGAATGTTGCTCCAGAGATCGGCTGTCTCCAAATTCAGCTTGAA---GAATTG 410
Db 261 GIuLeuGlyThraValMetArGserLeuGly-----Gln:snProThrGluAlaGluLeu 278
QY 409 GAGCCCTTAGTGGGAAAACCATGTTGAACCTTGATGATTCCTGTTCTTTATGATCC 350
Db 279 GlnaspMetIleasnGluValaIaspAlaaspGlyasnGlyThriIeTYrPheProGluPhe 298
QY 349 ATCTGAAACCACTGGACATGTGTGTGACGAAGAGAGAGAGAAATGTCATTCCAC 290
Db 299 LeuThraMetMetAlaArglySmetLyaspThra:spserGluGlu----- 314
QY 289 GCGGCGGTGAAGAGACAGTGCCTTGGCAAGCTTTAAAGTGTGATTCGATTCGAT 230
Db 315 -----IIea:rgluAlaPhearValPheaspIysasp 325
QY 229 GGGGATGGGTGGGGGATGTGAGAGCTTGAATACGTCTGGGAAGACTGGGATGTGA 170
Db 326 GIIAaNglyTYrIlse:raIlaIaGluLeuArGHIsValMetThra:snleugly----- 343
QY 169 GGTGAANAATGAGAAAACACGACGAGCATGATTTGGTATTACGACCAATTCAGAC 110
Db 344 GIuLyLeuThra:spgluValaIaspGluMetIIea:rgluAlaaspIleaspGlyasp 363
QY 109 GGCATGTTGATTTTCAGAAATTCAAAACATGATG 74
Db 364 GIyGlnVala:snTYrGluGluPheValGlnMetMet 375

Db 344 GIuLyLeuThra:spgluValaIaspGluMetIIea:rgluAlaaspIleaspGlyasp 363
QY 109 GGCATGTTGATTTTCAGAAATTCAAAACATGATG 74
Db 364 GIyGlnVala:snTYrGluGluPheValGlnMetMet 375

RESULT 10
US-08-818-253-4
; Sequence 4, Application US/08818253
; Patent No. 5988204
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Miyawaki, Atsushi
; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
; FILE REFERENCE: 07257/043001
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/818,253
; FILING DATE: 14-MAR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Halle, Ph.D., Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07257/043001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 652 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-818-253-4

Alignment Scores:
Pred. No.: 2,41e-08 Length: 652
Score: 147.00 Matches: 41
Percent Similarity: 50.66% Conservative: 36
Best Local Similarity: 26.97% Mismatches: 57
Query Match: 13.85% Indels: 18
Gaps: 4
DB: 2

US-10-021-323-13 (1-609) x US-08-818-253-4 (1-652)

QY 526 GACTTGCAACGCGTATTCGAGAACTCGACAAAGATGAGATGCTTGTAGCTGGAG 467
Db 241 GIuPheLySGluAlaPhe:serLeuPheaspIysaspGlyThriIeThra:Thryls 260
QY 466 GAGCTGAATGTTGCTCCAGAGATCGGCTGTCTCCAAATTCAGCTTGAA---GAATTG 410
Db 261 GIuLeuGlyThraValMetArGserLeuGly-----Gln:snProThrGluAlaGluLeu 278
QY 409 GAGCCCTTAGTGGGAAAACCATGTTGAACCTTGATGATTCCTGTTCTTTATGATCC 350
Db 279 GlnaspMetIleasnGluValaIaspAlaaspGlyasnGlyThriIeTYrPheProGluPhe 298
QY 349 ATCTGAAACCACTGGACATGTGTGTGACGAAGAGAGAGAGAAATGTCATTCCAC 290

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Db      229 LeuThrMetMetAlaArglyMetlysaSPThrAspSerGluGlu----- 314
      289 GGGGGCGGGAAGAGAAGAACAGTACCTTGGGAAGCTTTTAAAGTTTGAATTGAT 230
      315 -----11LeaGgLuAlaPheArgValPheAspLysAsp 325
Qy      229 GGGGATGGGTGGGGGATGTAGAGCTTGAATACCTGCTGGGAAGACTGGGTATGTGA 170
      326 G1yAsnGlyTyrIleSerAlaAlaGluLeuAlaGhIleValMetThrAsnLeuGly----- 343
Db      169 GGTGAATAAGTGAAGAAAGACTGCAGAGCATGATTTGGTATTACACCAATTTCAGAC 110
      344 G1uYsLeuThrAspGluGluValAspGluMetIleArgGluAlaAspIleAspGlyAsp 363
Qy      109 GGCATGTTGATTTTCAGAAATTCAAAAACATGATG 74
      364 GlyGlnValAsnTyrGluGluPheValGlnMetMet 375

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RESULT 11

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US-08-818-252-4
/ Sequence 4, Application US/08818252B
/ Patent No. 6197928
/ GENERAL INFORMATION:
/ APPLICANT: Tsien, Roger Y.
/ APPLICANT: Miyawaki, Atsushi
/ TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
/ TITLE OF INVENTION: DETECTION OF ANALYTES
/ FILE REFERENCE: 07257/042001
/ CURRENT APPLICATION NUMBER: US/08/818,252B
/ CURRENT FILING DATE: 1997-03-14
/ NUMBER OF SEQ ID NOS: 56
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 4
/ LENGTH: 652
/ TYPE: PRT
/ ORGANISM: Aequorea victoria
US-08-818-252-4

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Alignment Scores:

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Pred. No.: 2,41e-08 Length: 652
Score: 147.00 Matches: 41
Percent Similarity: 50.66% Conservative: 36
Best Local Similarity: 26.97% Mismatches: 57
Query Match: 13.85% Indels: 18
DB: Gaps: 4

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US-10-021-323-13 (1-609) x US-08-818-252-4 (1-652)

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Qy      526 GACTTGCAACGGGTATTGGAAGCTCGAAGAAATGAGATGGCTTCTTATGTCGAG 467
      241 G1uPheLysGluAlaPheSerIleuPheAspLysAspGlyAspGlyThrIleThrThrLys 260
Qy      466 GAGCTGAATGGTGTCTCCAGAGAAATCGGGTCTGTTCACATTCAGCTTGA--GAAATG 410
      261 G1uLeuGlyThrValMetArgSerIleuGly-----GlnAsnProThrGluAlaGluLeu 278
Db      409 GAGCCCTTAGTGGGAAAAACCATGTTGAACCTTGATGAATCTTGTCTTTATGAAATCC 350
      279 GlnAspMetCileAsnGluValAspAlaAspGlyAsnGlyThrIleTyrPheProGluPhe 298
Qy      349 ATCTGGAACCACTGGCACAATGCTGTGTGACGAAGAGAGAGAGAGATGTCATTGAC 290
      299 LeuThrMetMetAlaArglyMetLysAspThrAspSerGluGluGlu----- 314
Db      289 GCGCGGCGTGAAGAGAAGACAGTGAACCTTGCGAAGCGCTTTAAAGTGTGTAATTCAT 230
      315 -----11eArgGluAlaPheArgValPheAspLysAsp 325
Qy      229 GGGGATGGGTGGGGGATGTAGAGCTTGAATACCTGCTGGGAAGACTGGGTATGTGA 170
      326 G1yAsnGlyTyrIleSerAlaAlaGluLeuAlaGhIleValMetThrAsnLeuGly----- 343

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Qy      169 GGTGAATAAGTGAAGAAAGACTGCAGAGCATGATTTGGTATTACACCAATTTCAGAC 110
      344 G1uYsLeuThrAspGluGluValAspGluMetIleArgGluAlaAspIleAspGlyAsp 363
Qy      109 GGCATGTTGATTTTCAGAAATTCAAAAACATGATG 74
      364 GlyGlnValAsnTyrGluGluPheValGlnMetMet 375

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RESULT 12

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US-08-464-164-2
/ Sequence 2, Application US/08464164
/ Patent No. 5614195
/ GENERAL INFORMATION:
/ APPLICANT: Tomley, Fiona M.
/ APPLICANT: Dunn, Paul P. J.
/ APPLICANT: Bumstead, Janene M.
/ APPLICANT: Vermeulen, Arno N.
/ TITLE OF INVENTION: Coccidiosis poultry vaccine
/ NUMBER OF SEQUENCES: 10
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Akzo No. 5614195el Patent Department
/ STREET: 1300 Piccard Drive, Suite 206
/ CITY: Rockville
/ STATE: Maryland
/ COUNTRY: U.S.A.
/ ZIP: 20850
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/464,164
/ FILING DATE: June 2, 1995
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Gormley, Mary E.
/ REGISTRATION NUMBER: 34,409
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (301) 258-5200
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 456 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-464-164-2

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Alignment Scores:

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Pred. No.: 3,08e-08 Length: 456
Score: 145.50 Matches: 51
Percent Similarity: 41.18% Conservative: 26
Best Local Similarity: 27.27% Mismatches: 59
Query Match: 13.71% Indels: 51
DB: Gaps: 6

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US-10-021-323-13 (1-609) x US-08-464-164-2 (1-456)

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Qy      565 ATCTTGTGTGTGAATATGTCCTCCCTTAGTAAGACCGAC--TTCACACGCGTATTC 509
      290 LeuTyrMetGlySerLysLeuThrThrAsnGluGluValAspGluLeuAsnLysIlePhe 309
Qy      508 GAGAAGCTCGACAAAGAAATGAGATGGCTTGTGATCTGAGAGACTGAATTTGGTTCCTC 449
      310 G1uYsMetAspLysAsnGlyAspGlyGlnLeuAspLysGlnGluLeu----- 325
Db      448 CAGAGAATCGGCTGTGCAATTCAGCTTGAAGATTTGAGACCTTATGGGAAGAACCA 389
      326 -----MetGluGlyTyrValGluLeuMetLysLeuLysGlyGluAsp 339
Qy      388 TGTTTGAATCGATGAATTTCTTGTCTTTATGAATCAATCTCGAACCACTGCACAT 329
      340 ValSerValLeuAspLysSerAlaIle----- 348

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QY 328 GGTGTGACGAGAGAGAGAAATTCATTACAGC-----GGC 284
DB 349 -----GluThrGluValGluGluValLeuGluValAlaAspPheAspLysAsn 364
QY 283 GGTGAAGAAGACAGTGC----- 263
DB 365 GlyPheIleGluTyrSerGluPheValThrValAlaMetAspArgArgThrLeuSer 384
QY 262 -----CTTGCAGAGCTTTTAAAGCTTTGACTTAATGGGGATGGGTTGGGGGA 212
DB 385 ArgGlnArgLeuGlnArgAlaPheGluMetPheAspSerAspGlySerGlyLysIleSer 404
QY 211 TGTGAGAGCTTGAAATACGTCCTGGAGAGACTGGATGTGAGTGAATAATGTGGA 152
DB 405 SerSerGluLeuAlaThrIlePheGlyVal-----SerGluLeuAspSerGlu 420
QY 151 GACTGCAGAGACATGATTTGTATTACGACACCAATTCAGACGCGATGGTTGATTC 92
DB 421 AlaTPrArgArgValLeuAlaGluValAlaAspArgAsnAsnAspGlyGluValAspPheGlu 440
QY 91 GAATTCAAAACATGATGTTA 71
DB 441 GluPheGlnGluMetLeuLeu 447
RESULT 13
US-08-338-057-2
; Sequence 2, Application US/08338057
; Patent No. 5795741
; GENERAL INFORMATION:
; APPLICANT: Tomley, Fiona M.
; APPLICANT: Dunn, Paul P. J.
; APPLICANT: Bumstead, Janene M.
; APPLICANT: Vermeulen, Arno N.
; TITLE OF INVENTION: Coccidiosis poultry vaccine
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Organon Teknika Corporation
; STREET: 1330 Piccard Drive
; CITY: Rockville
; STATE: Maryland
; COUNTRY: U.S.A.
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/338,057
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93.309078.9
; FILING DATE: 12-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Gornley, Mary E.
; REGISTRATION NUMBER: 34,409
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 258-5200
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 456 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-338-057-2
Alignment Scores:
Pred. No.: 3.08e-08 Length: 456
Score: 145.50 Matches: 51
Percent Similarity: 41.18% Conservative: 26
Best Local Similarity: 27.27% Mismatches: 59

Query Match: 13.71% Indels: 51
DB: 1 Gaps: 6
US-10-021-323-13 (1-609) x US-08-338-057-2 (1-456)
QY 565 ATCTCTTGTGTGTGTAATATGTCCTCCCTTGTAGTAAAGCCAGC---TTGCACCGGTATTC 509
DB 290 LeuTyrMetGlySerLysLeuThrThrAsnGluGluThrAspGluLeuAsnLysIlePhe 309
QY 508 GAGAACTCGACAGAAATGATGATGCTGCTGCTGCTGAGAGAGCTGAATTTGTTGCTC 449
DB 310 GlnLysMetAspLysAsnGlyAspGlyGluLeuAspLysGlnGluLeu----- 325
QY 448 CAGAGAATCGGCTGTCCATTCAGCCTTGAAGATTTGAGCCCTTATGGGAAACCA 389
DB 326 -----MetGluGlyTyrValGluLeuMetLysLeuLysGlyGluAsp 339
QY 388 TGTTTGAACCTTGATGATTCCTTCTTTTATGAAATCCATTCGAAACCACTGGACAT 329
DB 340 ValSerValLeuAspLysSerAlaIle----- 348
QY 328 GGTGTGACGAGAGAGAGAGAGAAATTCATTACAGC-----GGC 284
DB 349 -----GluThrGluValGluGluValLeuGluValAlaAspPheAspLysAsn 364
QY 283 GGTGAAGAAGACAGTGC----- 263
DB 365 GlyPheIleGluTyrSerGluPheValThrValAlaMetAspArgArgThrLeuSer 384
QY 262 -----CTTGCAGAGCTTTTAAAGCTTTGACTTAATGGGGATGGGTTGGGGGA 212
DB 385 ArgGlnArgLeuGlnArgAlaPheGluMetPheAspSerAspGlySerGlyLysIleSer 404
QY 211 TGTGAGAGCTTGAAATACGTCCTGGAGAGACTGGATGTGAGTGAATAATGTGGA 152
DB 405 SerSerGluLeuAlaThrIlePheGlyVal-----SerGluLeuAspSerGlu 420
QY 151 GACTGCAGAGACATGATTTGTATTACGACACCAATTCAGACGCGATGGTTGATTC 92
DB 421 AlaTPrArgArgValLeuAlaGluValAlaAspArgAsnAsnAspGlyGluValAspPheGlu 440
QY 91 GAATTCAAAACATGATGTTA 71
DB 441 GluPheGlnGluMetLeuLeu 447
RESULT 14
US-08-668-416-2
; Sequence 2, Application US/08668416
; Patent No. 5843722
; GENERAL INFORMATION:
; APPLICANT: Tomley, Fiona M.
; APPLICANT: Dunn, Paul P. J.
; APPLICANT: Bumstead, Janene M.
; APPLICANT: Vermeulen, Arno N.
; TITLE OF INVENTION: Coccidiosis poultry vaccine
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Akzo No. 5843722el Patent Department
; STREET: 1300 Piccard Drive, Suite 206
; CITY: Rockville
; STATE: Maryland
; COUNTRY: U.S.A.
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/668,416
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

Mon Feb 2 08:52:48 2004

us-10-021-323-13.rtf

Page 10

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Search completed: January 31, 2004, 02:43:44
Job time : 22.5 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: January 31, 2004, 02:32:26 ; Search time 44.5 Seconds

(without alignments)
5688.308 Million cell updates/sec

Title: US-10-021-323-13

Perfect score: 1100

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Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 789580 segs, 207824079 residues

Total number of hits satisfying chosen parameters: 1579160

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=Published Applications_AA -OFMT=faстан -SUFFIX=rapb -MINMATCH=0.1
-LOOPEXT=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=bloumm62
-TRANS=human40.cdi -LIST=45 -DOCLIGN=200 -THR SCORE=pcpt -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=plc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US10021323@cgn_1.1.46@runat_30012004_112102_3623
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEOBJECT -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGIOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELXT=7

Database : Published Applications_AA:*

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3:	/cgn2_6/ptodata/2/pubpa/US06_NEW_PUB.pcp.*
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9:	/cgn2_6/ptodata/2/pubpa/US09_PUBCOMB.pcp.*
10:	/cgn2_6/ptodata/2/pubpa/US09C_PUBCOMB.pcp.*
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16:	/cgn2_6/ptodata/2/pubpa/US06_NEW_PUB.pcp.*
17:	/cgn2_6/ptodata/2/pubpa/US06_PUBCOMB.pcp.*
18:	/cgn2_6/ptodata/2/pubpa/US06_PUBCOMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 1	239.5	22.6	205	11	US-09-847-208-45	Sequence 45, Appl
C 2	204	19.2	145	12	US-10-369-493-5397	Sequence 5397, Ap
C 3	154	14.5	159	10	US-09-910-071-5	Sequence 5, Appl
C 4	152.5	14.4	160	12	US-10-176-416-1	Sequence 1, Appl
C 5	152.5	14.4	160	15	US-10-192-806-1	Sequence 1, Appl
C 6	152.5	14.4	160	15	US-10-286-134-1	Sequence 1, Appl
C 7	152	14.3	150	12	US-10-369-493-6776	Sequence 6776, Ap
C 8	147	13.9	642	10	US-09-554-000-2	Sequence 2, Appl
C 9	147	13.9	652	10	US-09-554-000-4	Sequence 4, Appl
C 10	146.5	13.8	218	12	US-10-369-493-6535	Sequence 6535, Ap
C 11	144	13.6	642	10	US-09-554-000-6	Sequence 6, Appl
C 12	144	13.6	656	10	US-09-554-000-8	Sequence 8, Appl
C 13	143	13.5	408	11	US-09-988-462-21	Sequence 21, Appl
C 14	143	13.5	464	11	US-09-988-462-22	Sequence 22, Appl
C 15	142	13.4	149	12	US-10-369-493-6260	Sequence 6260, Ap
C 16	142	13.4	416	11	US-09-989-025A-8	Sequence 8, Appl
C 17	141	13.3	148	11	US-09-989-025A-4	Sequence 4, Appl
C 18	141	13.3	149	12	US-10-341-434-105	Sequence 105, App
C 19	141	13.3	149	12	US-10-291-172-219	Sequence 219, App
C 20	141	13.3	149	15	US-10-177-293-35	Sequence 35, Appl
C 21	139.5	13.1	227	12	US-10-291-172-243	Sequence 243, App
C 22	138	13.0	136	12	US-10-342-324-60	Sequence 60, Appl
C 23	136.5	12.9	142	10	US-09-910-071-4	Sequence 4, Appl
C 24	136.5	12.9	957	12	US-10-259-165-252	Sequence 252, App
C 25	136	12.8	149	12	US-10-369-493-2146	Sequence 2146, Ap
C 26	133.5	12.5	187	12	US-10-259-165-4	Sequence 4, Appl
C 27	133.5	12.5	187	12	US-10-259-165-358	Sequence 358, App
C 28	132	12.4	142	11	US-09-988-462-24	Sequence 24, Appl
C 29	130.5	12.3	501	12	US-10-289-172-3	Sequence 3, Appl
C 30	130.5	12.3	501	12	US-09-848-806-3	Sequence 3, Appl
C 31	128.5	12.1	163	11	US-09-764-881-126	Sequence 126, App
C 32	128.5	12.1	163	12	US-10-242-747-126	Sequence 126, App
C 33	128.5	12.1	163	12	US-10-158-057-305	Sequence 305, App
C 34	127.5	12.0	146	15	US-10-157-031-295	Sequence 295, App
C 35	127	12.0	160	12	US-10-369-493-5550	Sequence 5550, App
C 36	123	11.6	141	12	US-10-369-493-19795	Sequence 19795, A
C 37	121.5	11.5	163	12	US-10-320-797-3020	Sequence 3020, Ap
C 38	121.5	11.5	495	12	US-10-289-172-1	Sequence 1, Appl
C 39	121.5	11.5	495	12	US-09-848-806-1	Sequence 1, Appl
C 40	120.5	11.4	371	12	US-10-353-826-9	Sequence 9, Appl
C 41	120.5	11.4	390	12	US-10-353-826-4	Sequence 4, Appl
C 42	118	11.1	639	10	US-09-854-731-17	Sequence 17, Appl
C 43	117.5	11.1	167	15	US-10-128-714-8159	Sequence 8159, Ap
C 44	117	10.6	258	12	US-10-104-047-3034	Sequence 3034, Ap
C 45	117	11.0	549	12	US-10-259-194A-258	Sequence 258, App

ALIGNMENTS

RESULT 1
US-09-847-208-45
; Sequence 45, Application US/09847208
; Publication No. US20030082190A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; APPLICANT: Zhu, Daocheng
; TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
; TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES
; FILE REFERENCE: UC67.002A
; CURRENT APPLICATION NUMBER: US/09/847.208
; CURRENT FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; TYPE: PRT
; ORGANISM: Betula verrucosa (White birch) (Betula pendula)
US-09-847-208-45

Alignment Scores: 1.73e-16 Length: 205
Pred. No.: 239.50 Matches: 63
Score:

Percent Similarity:	57.93%	Conservative:	32
Best Local Similarity:	38.41%	Mismatches:	58
Query Match:	22.57%	Indels:	6
DB:	11	Gaps:	11

US-10-021-323-13 (1-609) X US-09-847-208-45 (1-205)

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Oy 538 CTTAGTAAAGACCCAGCTATTCGCAACCGCTATTCGAGAGCTCCAGAAATGAGAGTGGCTTC 479
Db 36 LeuAenThlrLeuAargLeuAargArgIlePheAaspLeuAheAapLyAaenSerAaspIlylle 55
Oy 478 GTTAGCTCTGAGAGAGCTGTAATGGTCTCCAGAAATCGGAGTCTGTCCAAATTCAGCCTT 419
Db 56 IleThValAaspIleuSerAArgAlaLeuAenLeuEngly---LeuGluThrAaspLeu 74
Oy 418 GAAGAATTGAGCGCTTAGTG-----GGAAACCATGTTTGAACTTG 377
Db 75 SerGluLeuGlnSerThrValLySerPheThrArgGluGluAenIleGlyLeuGlnPhe 94
Oy 376 GATGAATTCTTGTCTTTTATGAATTCATCTCGAACCA---CTGGACATGGTGT--- 323
Db 95 GluAaspPheIleSerLeuHISGlnSerLeuAaAaspertyrPheAlatyGlyGlyu 114
Oy 322 GACGAGAGAGAGAGAGCAATGGTCAATTCACGCGCGGTGAAGAAGAGAGAGTAC 263
Db 115 AaPglAaAaspAaenGluGluAaPmeAArgLySerIleuSerGlnGluGluAasp 134
Oy 262 CTTGCGAAGGCTTTTAAAGTGTTCAGCTTAATGAGGAGATGGGTTGGGGGAGATGTGAGAG 203
Db 135 SerPheGlyGlyPheLySerValPheAaspGluAaspGlyTyrIleSerAlaArgIlu 154
Oy 202 CTTGAATAGCTGCTGGAGAGACTGGATGTGAGAGTAAAAATAGTGAAGAAGAC---TGC 146
Db 155 LeuGlnMetValLeuGlyLySerLeuGlyPhe---SerGluGlySerGluIleAaspArgVal 173
Oy 145 AGAGAGCATGATTTGGTATTACGACACCAATTCAGACGGCATGTGATTTTCAAGAAATTC 86
Db 174 GluLyMetCilleValSerValAaspSerAaAaArgAaspGlyArgValAaPhePheGluPhe 193
Oy 85 AAAAACAATGATG 74
Db 194 LyAaPmeCmet 197

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RESULT 2
US-10-369-493-5397
; Sequence 5397, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 5397
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-5397

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Conservative:	36
Mismatches:	30
Indels:	49

DB:	12	Gaps:	5
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RESULT 3
US-09-910-071-5
: Sequence 5, Application US/09910071
: Patent No. US2002011616A1
: GENERAL INFORMATION:
: APPLICANT: Tomikawa, Mayumi
: APPLICANT: Aikawa, Seichi
: APPLICANT: Matsuzawa, Fumiko
: TITLE OF INVENTION: Method and Apparatus for Extracting and Evaluating Mutually Similar
: TITLE OF INVENTION: Portions in One-Dimensional Sequences in Molecules and/or Three-
: TITLE OF INVENTION: Structures of Molecules
: FILE REFERENCE: 522.1921D2
: CURRENT APPLICATION NUMBER: US/09/910,071
: CURRENT FILING DATE: 2001-07-23
: PRIOR APPLICATION NUMBER: US 08/014,867
: PRIOR FILING DATE: 1993-02-08
: NUMBER OF SEQ ID NOS: 20
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 5
: LENGTH: 159
: TYPE: PRT
: ORGANISM: unknown
: FEATURE:
: OTHER INFORMATION: Figure 23B
US-09-910-071-5

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Best Local Similarity:	28.03%
Query Match:	14.51%
DB:	10
Length:	159
Matches:	44
Conservative:	27
Mismatches:	26
Indels:	5
Gaps:	2

US-10-021-323-13 (1-609) x US-09-910-071-5 (1-159)

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Db 19 GlnpHeuYAlaAlaPhaSpMetPheAspAlaAspGlyGlyAspIleSerThrLys 38
QY 466 GAGCTGAATTTGGTCTCCAGAGATCGGGTCTGTCCATTCAGCTTGAAGATTTGAG 407
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QY 364 TTCCTTTATGATTCATCTCGAACCCACTGACATGCTGTGTGAGAGAGAGAGAGAG 305
Db 78 ValMetValArgGluMetLysGluAsp--AlaLysGlyLysSerGluGluGln----- 94
QY 304 GAATTGTCATTCACGGCGCGGTGAAGAGACAGTGAACCTTGCGAAGGCTTTTAA 245
Db 95 -----LeuAlaAspCysPheArg 100
QY 244 GTGTTGACTTGAATGCGGATGCGGTGGCGGATGTGAGAGCTTGAATACGTCGTGGA 185
Db 101 IlePheAspLysAsnAlaAspGlyPheIleAspIleGluGluLeuGlyGluIleLeuArg 120
QY 184 AGACTGGGTATGTGAGCTGAAAAATAGTGAAGAAAGACTGACAGAGCATGATTGTATTAC 125
Db 121 AlaThrGly-----GluHisValThrGluGluAspIleGluAspLeuMetLysAspSer 138
QY 124 GACACCAATTCAGACGGCATGTTGATTTTCAGAAATTCAAAAACATGATG 74
Db 139 AspLysAsnAsnAspGlyArgIleAspPheAspGluPheLeuLysMetMet 155

RESULT 4
US-10-176-416-1
; Sequence 1, Application US/10176416
; Publication No. US20030186864A1
; GENERAL INFORMATION:
; APPLICANT: Thorm, R.
; APPLICANT: Lanzer, M.
; APPLICANT: Moses, M.
; APPLICANT: Wiederschain, D.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS COMPRISING TROPONIN SUBUNITS.
; TITLE OF INVENTION: INHIBIT ANGIOGENESIS
; FILE REFERENCE: 8657-043
; CURRENT APPLICATION NUMBER: US/10176,416
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: 09/442,099
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 09/268,274
; PRIOR FILING DATE: 1999-03-15
; PRIOR APPLICATION NUMBER: 08/961,264
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: 08/602,941
; PRIOR FILING DATE: 1996-02-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-176-416-1

Alignment Scores:
Pred. No.: 2,65e-07 Length: 160
Score: 152.50 Matches: 43
Percent Similarity: 45.86% Conservative: 29
Best Local Similarity: 27.39% Mismatches: 60
Query Match: 14.37% Indels: 25
DB: 12 Gaps: 4

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US-10-021-323-13 (1-609) x US-10-176-416-1 (1-160)

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QY 526 GACCTGCAACGGGTATTCGAGAGCTCGACAAAGATGAGATGCTTGTAGTCTGAG 467
Db 19 GlnpHeuYAlaAlaPhaSpMetPheAspAlaAspGlyGlyAspIleSerThrLys 38
QY 466 GAGCTGAATTTGGTCTCCAGAGATCGGGTCTGTCCATTCAGCTTGAAGATTTGAG 407
Db 39 GluLeuGlyThrValMetArgMetLeuGlyGlnThrPro--ThrLysGluGluLeuAsp 57
QY 406 CCCTTAGTG-----GGAACCACTGTTGAATTCGATGATGATTTCTTG 365
Db 58 AlaIleIleGluGluValAspGluAspGlySerGlyThrIleAspHeuGluGluPheLeu 77
QY 364 TTCCTTTATGATTCATCTCGAACCCACTGACATGCTGTGTGAGAGAGAGAGAGAG 305
Db 78 ValMetValArgGluMetLysGluAspAlaLysGlyLysSerGluGluGln----- 95
QY 304 GAATTGTCATTCACGGCGCGGTGAAGAGACAGTGAACCTTGCGAAGGCTTTTAA 245
Db 96 -----LeuAlaGluCysPheArg 101
QY 244 GTGTTGACTTGAATGCGGATGCGGTGGCGGATGTGAGAGCTTGAATACGTCGTGGA 185
Db 102 IlePheAspArgAsnAlaAspGlyThrIleAspProGluGluLeuAlaGluIlePheArg 121
QY 184 AGACTGGGTATGTGAGCTGAAAAATAGTGAAGAAAGACTGACAGAGCATGATTGTATTAC 125
Db 122 AlaSerGly-----GluHisValThrAspGluGluIleGluSerLeuMetLysAspGly 139
QY 124 GACACCAATTCAGACGGCATGTTGATTTTCAGAAATTCAAAAACATGATG 74
Db 140 AspLysAsnAsnAspGlyArgIleAspPheAspGluPheLeuLysMetMet 156

RESULT 5
US-10-192-806-1
; Sequence 1, Application US/10192806
; Publication No. US20030083255A1
; GENERAL INFORMATION:
; APPLICANT: Thorm, R.
; APPLICANT: Lanzer, M.
; APPLICANT: Moses, M.
; APPLICANT: Wiederschain, D.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS COMPRISING
; TITLE OF INVENTION: TROPONIN SUBUNITS, FRAGMENTS AND HOMOLOGS THEREOF AND
; TITLE OF INVENTION: METHODS OF THEIR USE TO INHIBIT ANGIOGENESIS
; FILE REFERENCE: 8657-042-999
; CURRENT APPLICATION NUMBER: US/10192,806
; CURRENT FILING DATE: 2002-07-09
; PRIOR APPLICATION NUMBER: 09/612,421
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 09/268,274
; PRIOR FILING DATE: 1999-03-15
; PRIOR APPLICATION NUMBER: 08/961,264
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: 08/602,941
; PRIOR FILING DATE: 1996-02-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-192-806-1

Alignment Scores:
Pred. No.: 2,65e-07 Length: 160
Score: 152.50 Matches: 43
Percent Similarity: 45.86% Conservative: 29
Best Local Similarity: 27.39% Mismatches: 60
Query Match: 14.37% Indels: 25
DB: 15 Gaps: 4

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Db      53 SerProthGluAspGluLeuAspAlaMetPheGlnAlaAspIleAspCysAspGly 72
Qy      385 ---TTGAAGCTGGATTAATCTGTTCTTTATGATTCATCGAAGCCACCGACAT 329
Db      73 AmlIleAspPheGlnIleuPheValIleAlaIleS---AlaAsnProLeuSer--- 89
Qy      328 GGTGTGACGAAGAGAGAGAGAGAAATGTCATTCACGGCGCGGTGAAGAAGAAC 269
Db      89 ----- 89
Qy      268 AGTGACCTTGCCAGAGCTTTTAAGTCTTTGACTGATGAGGATGGTGGGGGATG 209
Db      90 LeuSerLeuIleValAlaValPheGlnGluLeuAspValAspGlyIleThrArg 109
Qy      208 GAGGAGCTTGATACGTCGTCGGAGAGCTGGGATGATGAGGTAATGAGAAAGAC 149
Db      110 SerGluLeuArgThrAlaPheGlnArgMetGly-----HisSerLeuSerAspGlnAsp 127
Qy      148 TGCAGAGAGCATGATTTGTGTAATACGACACCAATTCAGACGCGATGTTGATTTCA 92
Db      128 IleValAlaIleTyrArgHisValAspGlnAsnAsnAspGlyLysIleAsnPheGln 146

RESULT 8
US-09-554-000-2
; Sequence 2, Application US/09554000
; Patent No. US20020165364A1
; GENERAL INFORMATION:
; APPLICANT: Taisen, Roger Y.
; APPLICANT: Miyawaki, Atsushi
; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
; FILE REFERENCE: 07257/042001
; CURRENT APPLICATION NUMBER: US/09/554,000
; PRIORITY FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 08/818,252
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 642
; TYPE: PRF
; ORGANISM: Aequorea victoria
US-09-554-000-2

Alignment Scores:
Pred. No.: 1,58e-06 Length: 642
Score: 147.00 Matches: 41
Percent Similarity: 50.66% Conservative: 36
Best Local Similarity: 26.97% Mismatches: 57
Query Match: 13.85% Indels: 18
DB: 10 Gaps: 4

US-10-021-323-13 (1-609) x US-09-554-000-2 (1-642)
Qy      526 GACTTCAACGCGTATTTCGAGAAGCTCGACAAGATGAGATGCTTGTATGCTGAG 467
Db      241 GlnPheIleGluAlaPheSerLeuPheAspIleAspGlyThrIleThrArgLys 260
Qy      466 GAGCTGAATGTTGCTCCAGAGAAATCGGCTCTGTCCAATTCAGCCTTGA---GAATTG 410
Db      261 GluLeuGlyThrValMetArgSerLeuGly-----GlnAsnProThrGlnAlaGluLeu 278
Qy      409 GAGCCCTTAGTGGGAAAACATCTTGAACCTTGAGATGATCTTGTCTTTATGATTC 350
Db      279 GlnAspMetIleAsnGluValAspAlaAspGlyAsnGlyThrIleTyrPheProGluPhe 298
Qy      349 ATCTGAAACCACTGCGACATGCTGTGACGAAGAGAGAGAGAAATGTCATTAC 290
Db      299 LeuThrMetMetAlaArgLysMetLysAspThrAspSerGluGluIle----- 314
Qy      289 GGGGGGGTGAAGAAGACAGTGAACCTTGCAAGGCTTTTAAGTGTGTTGCTTGAAT 230

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Db      315 -----IleArgGluAlaPheArgValPheAspIleAsp 325
Qy      229 GGGATGGTGGTGGGGGATGTGAGAGCTTGAAATACGTGCTGGGAAGACTGGGTATGCA 170
Db      326 GlyAsnGlyTyrIleSerAlaAlaGluLeuArgHisValMetThrAsnLeuGly----- 343
Qy      169 GGTGAATAATAGTGAAGAAAGACTCGAGAGCATGATTTGTGATTTACACCAATTCAGAC 110
Db      344 GluIleLeuThrAspGluGluValAspGluMetIleArgGluAlaAspIleAspGlyAsp 363
Qy      109 GGCATGTTGATTTCAAGAAATTCAAAACATGAAAG 74
Db      364 GlyGlnValAsnTyrGluGluPheValGlnMetMet 375

RESULT 9
US-09-554-000-4
; Sequence 4, Application US/09554000
; Patent No. US20020165364A1
; GENERAL INFORMATION:
; APPLICANT: Taisen, Roger Y.
; APPLICANT: Miyawaki, Atsushi
; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
; FILE REFERENCE: 07257/042001
; CURRENT APPLICATION NUMBER: US/09/554,000
; PRIORITY FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 08/818,252
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 652
; TYPE: PRF
; ORGANISM: Aequorea victoria
US-09-554-000-4

Alignment Scores:
Pred. No.: 1,59e-06 Length: 652
Score: 147.00 Matches: 41
Percent Similarity: 50.66% Conservative: 36
Best Local Similarity: 26.97% Mismatches: 57
Query Match: 13.85% Indels: 18
DB: 10 Gaps: 4

US-10-021-323-13 (1-609) x US-09-554-000-4 (1-652)
Qy      526 GACTTCAACGCGTATTTCGAGAAGCTCGACAAGATGAGATGCTTGTATGCTGAG 467
Db      241 GlnPheIleGluAlaPheSerLeuPheAspIleAspGlyThrIleThrArgLys 260
Qy      466 GAGCTGAATGTTGCTCCAGAGAAATCGGCTCTGTCCAATTCAGCCTTGA---GAATTG 410
Db      261 GluLeuGlyThrValMetArgSerLeuGly-----GlnAsnProThrGlnAlaGluLeu 278
Qy      409 GAGCCCTTAGTGGGAAAACATCTTGAACCTTGAGATGATCTTGTCTTTATGATTC 350
Db      279 GlnAspMetIleAsnGluValAspAlaAspGlyAsnGlyThrIleTyrPheProGluPhe 298
Qy      349 ATCTGAAACCACTGCGACATGCTGTGACGAAGAGAGAGAGAAATGTCATTAC 290
Db      299 LeuThrMetMetAlaArgLysMetLysAspThrAspSerGluGluIle----- 314
Qy      289 GGGGGGGTGAAGAAGACAGTGAACCTTGCAAGGCTTTTAAGTGTGTTGCTTGAAT 230
Db      315 -----IleArgGluAlaPheArgValPheAspIleAsp 325
Qy      229 GGGATGGTGGTGGGGGATGTGAGAGCTTGAAATACGTGCTGGGAAGACTGGGTATGCA 170
Db      326 GlyAsnGlyTyrIleSerAlaAlaGluLeuArgHisValMetThrAsnLeuGly----- 343
Qy      169 GGTGAATAATAGTGAAGAAAGACTCGAGAGCATGATTTGTGATTTACACCAATTCAGAC 110
Db      344 GluIleLeuThrAspGluGluValAspGluMetIleArgGluAlaAspIleAspGlyAsp 363
Qy      169 GGTGAATAATAGTGAAGAAAGACTCGAGAGCATGATTTGTGATTTACACCAATTCAGAC 110
Db      344 GluIleLeuThrAspGluGluValAspGluMetIleArgGluAlaAspIleAspGlyAsp 363

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QY 109 GGCATGTTGATTTTCAGAAATTCAAAACATGATG 74
DB 364 GlyGlnValAsnTyrGluGluPheValGlnMetMet 375

RESULT 10
US-10-369-493-6535
; Sequence 6535, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT FILING DATE: 2003-02-28
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/360,039
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6535
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6535

Alignment Scores:
Pred. No.: 1,266-06 Length: 218
Score: 146.50 Matches: 42
Percent Similarity: 42.29% Conservative: 32
Best Local Similarity: 24.00% Mismatches: 52
Query Match: 13.81% Indels: 49
DB: 12 Gaps: 4

US-10-021-323-13 (1-609) x US-10-369-493-6535 (1-218)
QY 550 AAAATGTCCTCCCTTAGTGAAGCCGCTTTCGAGAAAGCTGCACAAGAT 491
DB 74 GlnLeuThrProGluGlnIleAspGluPheArgGluAlaPheMetMetPheAsp 93
QY 490 GAGATGCTGCTGTTGCTGAGGAGCTGAATGGTCTCAGAGAACTGGCTCTGC 431
DB 94 GlyAsnGlyThrIleSerThrIleGluGlyIleAlaMetArgSerIleGlnAsn 113
QY 430 CAATTCAGCTTGAAGAAATTTGAGCCCTTAGTGGGAAAACATGTTGAATTTGATGAA 371
DB 114 ProThrGluGlnGluIleLeuGluMetIle----- 123
QY 370 TTCTGTTCTTTTAAATTCATCTTCGAACCACTGCGACATGCTGCTGACGAAGAGAG 311
DB 123 ----- 123
QY 310 GAGGAGAAATGATTCATTCACGCGCGCGGTAA----- 278
DB 124 ---AsnGlnValAspIleAspGlyAsnGlyGlnIleGluPheProGluPheCysValMet 142
QY 277 -----GAGAGAGACAGTGAACCTTTCGAGAG-----GCTTTTAAAGTGT 239
DB 143 MetLysArgMetMetLysGluThrAspSerGluMetIleArgGluAlaPheArgValPhe 162
QY 238 GACTTGAATGGGAGATGGTGGGGGAGATGAGAGCTTGAATACGCTGCTGGGAAAGACTG 179
DB 163 AspLysAspGlyAsnGlyValIleThrAlaGlnGluPheArgTyrPheMetValHisMet 182
QY 178 GGTATGTAGCGTGAATAATGTGAAAGACTGACAGAGAGCATTTGTGATTAACAGACC 119
DB 183 GlyMet-----GlnHisSerGluGluGluValAspGluMetIleLysGluValAspVal 200
QY 118 AATTCAGACGCGATGTTGATTTTCAGAAATTCAAAACATGATG 74
DB 118 ----- 118

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DB 201 AspGlyAspGlyGluIleAspTyrGluGluPheValLysMetMet 215

RESULT 11
US-09-554-000-6
; Sequence 6, Application US/09554000
; Patent No. US20020165364A1
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Miyawaki, Atsushi
; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
; TITLE OF INVENTION: DETECTION OF ANALYTES
; FILE REFERENCE: 07257/042001
; CURRENT FILING DATE: 2000-04-20
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 09/818,252
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 642
; TYPE: PRT
; ORGANISM: Aequorea victoria
US-09-554-000-6

Alignment Scores:
Pred. No.: 3,296-06 Length: 642
Score: 144.00 Matches: 40
Percent Similarity: 50.66% Conservative: 37
Best Local Similarity: 26.32% Mismatches: 57
Query Match: 13.57% Indels: 18
DB: 10 Gaps: 4

US-10-021-323-13 (1-609) x US-09-554-000-6 (1-642)
QY 526 GACTTCACACCGCATTCGAGAACGCTGCACAAGATGAGATGGCTTCCTGATCTGAG 467
DB 241 GluPheLysGluAlaPheSerLeuPheAspLysAspGlyAspGlyThrIleThrThrLys 260
QY 466 GAGCTGAATTTGGTCTCCAGAGAAATGGGCTCTCCCAATTCAGCTTGA-----GAATG 410
DB 261 GluLeuGlyThrValMetArgSerLeuGly-----GlnAsnProThrGluAlaGluLeu 278
QY 409 GAGCCTTAGTGGGAAAACCATGTTTGAACCTTGAATTCCTGTTTAAATGATCC 350
DB 279 GlnAspMetIleAsnGlnValAspAlaAspGlyAsnGlyThrIleThrPheProGluPhe 298
QY 349 ATTCGAAACCATGCGACATGCTGTCGACGAAGAGAGAGAGAAATGGCTATTGAC 290
DB 299 LeuThrMetMetAlaArgLysMetLysAspThrAspSerGluGluGlu----- 314
QY 289 GCGCGCGGTGAAGAAAGACAGTGCAGCTTCGGAAGCTTTTAAAGTGTGACTTGAAT 230
DB 315 -----IleArgGluAlaPheArgValPheAspLysAsp 325
QY 229 GGGATGGGTTGGGGGAGATGAGAGAGCTTGAATACGCTGCTGGAAGACTGGTATGTA 170
DB 326 GlyAsnGlyThrIleSerAlaAlaGlnLeuArgHisValMetThrAsnLeuGly----- 343
QY 169 GGTGAATAATAGTGAAGAAAGACTGACAGAGCATGATTTGTGATTAACGACCAATTCAGAC 110
DB 344 GluLysLeuThrAspGluGluValAspGluMetIleArgGluAlaAspIleAspGlyAsp 363
QY 109 GGCATGTTGATTTTCAGAAATTCAAAACATGATG 74
DB 364 GlyGlnValAsnTyrGluGluPheValGlnMetMet 375

RESULT 12
US-09-554-000-8
; Sequence 8, Application US/09554000
; Patent No. US20020165364A1
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Miyawaki, Atsushi

```


QY 280 GAAGAAGACAGTGCCTTGCAGAGCTTTAAAGTTGACTTGAATGGGATGG 221
Db 323 LeuAspArgGluGlnHisLeuTyrThrAlaPheGlnTyrPheAspIysAspAsnSergly 342
QY 220 TTGGGGGGATGTGAGAGCTTGAATACGTCGTGGGAAGCTGGTATGAGAGTAAAT 161
Db 343 TyrIleThrLysGluGlnLeuGlnHisAlaLeuLysGluGlnGlyLeuTyrAspAlaAsp 362
QY 160 AGTGAAGAAAGCTGCAGACATGATTTGTATTACGACCAATTACAGCGCATGTT 101
Db 363 LysIleLysAsp-----IleIleSerAspAlaAspSerAspAsnAspIlyArgIle 379
QY 100 GATTTTCAAGAAATTCAAAACATGATG 74
Db 380 AspTyrSerGluPheValAlaIleMetMet 388

RESULT 14

US-09-988-462-22
Sequence 22, Application US/09988462
Publication No. US20030046726A1
GENERAL INFORMATION:
APPLICANT: Kozziel, Michael G.
Deeaj, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Launis, Karen L.

TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
INSECTICIDAL ACTIVITY IN MAIZE

NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:

ADDRESSER: Syngenta Biotechnology, Inc.
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/988,462
FILING DATE: 20-NO. US20030046726A1-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/547,422
FILING DATE: 11-APR-2000
APPLICATION NUMBER: US 08/459,504
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-188051
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689

INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:

LENGTH: 464 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

HYPOTHETICAL: NO
FEATURE:
NAME/KEY: Protein
LOCATION: 1..464
OTHER INFORMATION: /note= "derived protein sequence of
pollen specific CDPK as disclosed in Figure 34."
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-988-462-22

Alignment Scores:

Pred. No.:	3,79e-06	Length:	464
Score:	143.00	Matches:	45
Percent Similarity:	44.97%	Conservative:	31
Best Local Similarity:	26.63%	Mismatches:	63
Query Match:	13.48%	Indels:	30
DB:	11	Gaps:	4

US-10-021-323-13 (1-609) x US-09-988-462-22 (1-464)

QY 562 CTCCTTGTGGTGAATAATGCCCCCTTAGTAAGACCGACTTGACACCGCTATTCGAGAAG 503
Db 306 IleIleIleAglGlyCyLeuSerGluGlnGluIleThrGlyLeuLysGluMetPheLysAsn 325
QY 502 CTCGACAAAGATGAGATGCTTGTGATGTTGAGAGAGCTGAATTGCTCTCCAGAA 443
Db 326 IleAspLysAspAsnSerglyThrIleThrLeuAspGluLeuLysHisGlyLeuAlaLys 345
QY 442 ATCGGCTGTCCCAATTCAGCCTTGAGAAATTCGAGCCCTTAGG----- 398
Db 346 HisGlyPro--LysLeuSerAspSerGluMetGluLysLeuMetGluAlaAlaAspAla 364
QY 397 ---GAAAACCATGTTGATGATGATGATCTTGTCTTTTATGATTCATCTCGAAC 341
Db 365 AspGlyAsnGlyLeuIleAspTyrAspGluPheVal----- 376
QY 340 CCACTGCGACATGCTGTGACGAAGAAGAGAGAGAGATTCATTCACGCGCGCT 281
Db 377 -----ThralaThrValHisMetAsnLys 384
QY 280 GAAGAAGACAGTGCCTTGCAGAGCTTTAAAGCTTGAATGGGATGG 221
Db 385 LeuAspArgGluGlnHisLeuTyrThrAlaPheGlnTyrPheAspIysAspAsnSergly 404
QY 220 TTGGGGGGATGTGAGAGCTTGAATACGTCGTGGGAAGCTGGTATGAGAGTAAAT 161
Db 405 TyrIleThrLysGluGlnLeuGlnHisAlaLeuLysGluGlnGlyLeuTyrAspAlaAsp 424
QY 160 AGTGAAGAAAGCTGCAGACATGATTTGTATTACGACCAATTACAGCGCATGTT 101
Db 425 LysIleLysAsp-----IleIleSerAspAlaAspSerAspAsnAspIlyArgIle 441
QY 100 GATTTTCAAGAAATTCAAAACATGATG 74
Db 442 AspTyrSerGluPheValAlaIleMetMet 450

RESULT 15.

US-10-369-493-6260
Sequence 6260, Application US/10369493
Publication No. US2003023675A1
GENERAL INFORMATION:

APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493

PRIOR FILING DATE: 2003-02-28
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

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; SEQ ID NO 6260
;
; LENGTH: 149
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; TYPE: PRF
; ORGANISM: Caenorhabditis elegans
;
US-10-369-493-6260

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Alignment Scores:

Pred. No.:	3.52e-06	Length:	149
Score:	142.00	Matches:	42
Percent Similarity:	48.10%	Conservative:	34
Best Local Similarity:	26.58%	Mismatches:	52
Query Match:	13.38%	Indels:	30
DB:	12	Gaps:	6

US-10-021-323-13 (1-609) x US-10-369-493-6260 (1-149)

[illegible]

Search completed: January 31, 2004, 02:46:06
Job time : 50.5 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Comphen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 31, 2004, 00:30:10 ; Search time 61 Seconds

(without alignments)
4406.596 Million cell updates/sec

Title: US-10-021-323-13

Perfect score: 609

Sequence: 1 ggaatgaatcaacattt.....tgaagcttacaattaag 609

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

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4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/ECTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	51.6	8.5	7218	1	US-08-232-463-14
2	40	6.6	1052	1	US-08-466-603-1
3	40	6.6	1052	1	US-08-314-503A-1
4	40	6.6	1052	1	US-08-468-066-1
5	40	6.6	1052	2	US-08-466-717-1
6	40	6.6	1052	3	US-08-466-743-1
7	40	6.6	1052	5	PCT-US95-12414-1
8	39.8	6.5	289	3	US-09-007-005-17
9	39.8	6.5	289	3	US-09-244-796-17
10	37.8	6.2	966	2	US-08-766-738-2
11	37.8	6.2	966	4	US-09-262-610-2
12	36.2	5.9	1965	3	US-09-178-252-26
13	35.6	5.8	3211	2	US-08-574-959A-8
14	35.6	5.8	3211	3	US-09-357-014-8
15	35.6	5.8	3901	2	US-08-574-959A-6
16	35.6	5.8	3901	3	US-09-357-014-6
17	35.4	5.8	3489	2	US-08-728-323A-1
18	35.4	5.8	3489	4	US-09-298-568-1
19	35.4	5.8	3489	4	US-09-410-399-1
20	35.4	5.8	32207	2	US-08-770-379-20
21	35.4	5.8	32207	3	US-08-757-669A-20
22	35.4	5.8	32207	4	US-09-230-371A-20
23	34.4	5.6	856	4	US-09-171-517B-15
24	34.4	5.6	4161	4	US-09-185-244-8
25	34.4	5.6	4161	4	US-09-471-913-1
26	34.4	5.6	12241	4	US-09-948-138-4
27	34.4	5.6	13737	4	US-09-538-414-10

28	33.6	5.5	2082	3	US-09-440-325A-2	Sequence 2, Appl1
29	33.6	5.5	2082	4	US-09-846-936A-2	Sequence 2, Appl1
30	33.6	5.5	7183	4	US-09-081-149-9	Sequence 9, Appl1
31	33.6	5.5	7183	4	US-09-081-149-10	Sequence 10, Appl1
32	33.4	5.5	2277	1	US-08-676-967-2	Sequence 2, Appl1
33	33.4	5.5	2277	1	US-08-676-967-2	Sequence 2, Appl1
34	33.4	5.5	2277	2	US-09-098-487-2	Sequence 6, Appl1
35	33.2	5.5	3624	2	US-07-951-715A-6	Sequence 2, Appl1
36	33.2	5.5	3624	2	US-08-459-448A-6	Sequence 6, Appl1
37	33.2	5.5	3624	3	US-08-459-448A-6	Sequence 6, Appl1
38	33.2	5.5	3624	3	US-08-459-448A-6	Sequence 6, Appl1
39	33.2	5.5	3624	3	US-08-459-448A-6	Sequence 6, Appl1
40	33.2	5.5	3624	3	US-09-053-549-7	Sequence 7, Appl1
41	33.2	5.5	3624	4	US-09-547-422-6	Sequence 6, Appl1
42	33.2	5.5	7001	1	US-08-258-261B-1	Sequence 1, Appl1
43	33.2	5.5	7001	1	US-08-456-837-1	Sequence 1, Appl1
44	33.2	5.5	7001	1	US-08-457-342-1	Sequence 1, Appl1
45	33.2	5.5	7001	1	US-08-457-646A-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1
US-08-232-463-14
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHRIFFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSER: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-9300
TELEFAX: (703) 683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: PTZpT-Fls
US-08-232-463-14
Query Match 8.5%; Score 51.6; DB 1; Length 7218;

Best Local Similarity 3.8%; Pred. No. 1.2e-05;
Matches 15; Conservative 221; Mismatches 160; Indels 0; Gaps 0;

```
QY 140 GGTCTGACGATCTTTTCCATTTTACCTACATACCCAGCTTCCGACGATATTC 199
    |||
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1058 GCTTGCATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1117
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 200 AAGTCTTCACATCCGCCCAACCATTCATTAAGTCAAAACATTAAAGCTTGCC 259
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1118 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1177
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 260 AAGTCACTGCTCTTTCTTCAACGCGCGGTAATGACCAATTCCTCTCTCTTC 319
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1178 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1237
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 320 GTCACACACATGCGCAGTGGTGCAGATGATTCATTAAGAAACAGATTCACCA 379
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1238 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1297
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 380 GTTCAAAACATGTTTCCACTAAGGCTCAATTCCTTCAAGCTGAATGACAGACCC 439
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1298 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1357
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 440 GATCTCTGAGCAACCAATTCAGCTCTTCAAGACTTAAGCAAGCATCTCATCTTCTC 499
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1358 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1417
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 500 GAGCTTCTGATAGCGCTTGAAGTCTTACT 535
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1418 TTTTTTTTTTTTTTTTTTTTTTTTTTTTATCT 1453
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

RESULT 2

US-08-466-603-1/c
Sequence 1, Application US/08466603
Patent No. 5726018
GENERAL INFORMATION:
APPLICANT: Pasternack, Gary R.
APPLICANT: Kuhnajda, Francis P.
TITLE OF INVENTION: No. 5726018el Mammalian Protein Associated With
TITLE OF INVENTION: Uncontrolled Cell Division
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSER: Banner, Birch, McKie & Beckett
STREET: 1001 G Street, N.W.
CITY: Washington, D.C.
STATE: District of Columbia
COUNTRY: U.S.A.
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,603
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/314,503
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Posorske Bag., Laurence H.
REGISTRATION NUMBER: 34,698
REFERENCE/DOCKET NUMBER: 1107,47218
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 508-9153
TELEFAX: 202 508-9299
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1052 base pairs
TYPE: nucleic acid
STRANDEDNESS: double

TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 97..843
US-08-466-603-1

Query Match 6.6%; Score 40; DB 1; Length 1052;
Best Local Similarity 46.7%; Pred. No. 0.017;
Matches 127; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

```
QY 59 AGAAGGGAATGTAACATCATGTTTGAATCTTGAATAATCAACATGCGTGAAT 118
    |||
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 879 ACAATAGAAATTTTCAAAATAGTATTCATTCATGATCATCTTCTCTATCTTC 820
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 119 GGTGTGTAATACCAATATGATGCTCTGAGTCTTTTCACTAATTTTCACTCATAC 178
    |||
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 819 AGTTCTGTTTGGCTTCTGACCCCTTCTTCAACAGCTCTTCTCATCTTCTCCTC 760
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 179 CAGTCTCCGACGACGATTTAAGTCTCTACATCCGCCAACCATCCCATTCAGTC 238
    |||
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 759 GTCATCTACCTCTCCATCGTTATTAACCTTTCATCTCTCTCTCTCCATCAGTC 700
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 239 AAACATTTAAAGCTTTCGCAAGTCACTGCTTCTTCTTCTTCAACGCGCGGTAATGAC 298
    |||
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 699 CTCCTTTCACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 640
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 299 CAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 330
    |||
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 639 TTCACTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 608
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

RESULT 3

US-08-314-503A-1/c
Sequence 1, Application US/08314503A
Patent No. 5734022
GENERAL INFORMATION:
APPLICANT: Pasternack, Gary R.
APPLICANT: Kuhnajda, Francis P.
TITLE OF INVENTION: No. 5734022el Mammalian Protein Associated With
TITLE OF INVENTION: Uncontrolled Cell Division
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSER: Banner, Birch, McKie & Beckett
STREET: 1001 G Street, N.W.
CITY: Washington, D.C.
STATE: District of Columbia
COUNTRY: U.S.A.
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/314,503A
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Posorske Bag., Laurence H.
REGISTRATION NUMBER: 34,698
REFERENCE/DOCKET NUMBER: 1107,47218
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 508-9153
TELEFAX: 202 508-9299
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1052 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

MOLECULE TYPE: cDNA
ORIGINAL SOURCE: Homo sapiens
FEATURE: CDS
NAME/KEY: CDS
LOCATION: 97..843
US-08-314-503A-1

Query Match 6.6%; Score 40; DB 1; Length 1052;
Best Local Similarity 46.7%; Pred. No. 0.017;
Matches 127; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

QY 59 AGAAGGGAATGTAATCATCATGTTTGAATCTTGAATAACACGCGCTGAAATT 118
DB ACAATAGGAATTTTCAAAATAGTTATTCAGTATCATCTTCTCCCTCATCTTC 820
QY 119 GGTGCTGAATACGAATCATGCTCTGAGTCTTTTCCATTAATTTTCACTACATACC 178
DB 819 AGTTCTGCTTTCCCTTCTGACCCCTTCTTCCACCAAGCTCTTCTTCTTCTCTC 760
QY 179 CAGTCTCCGACGACGATTAATCAAGCTCCGACATCCCGACCATCCCATTTGAAGTC 238
DB 759 GTCACTTACCTCTCATGTTAATCACTTCTTCACTCTCTCTCTCTCTCTCTCTCT 700
QY 239 AAACACTTAAAGCCTTGCAGAGTCACTGCTTCTTCTTCAACGCGCGCGTGAATGAC 298
DB 699 CTCCTCTTCACT 640
QY 299 CAATTCCT 330
DB 639 TTCATCATCT 608

RESULT 4

US-08-468-066-1/c
Sequence 1, Application US/08468066
Patent No. 5756676

GENERAL INFORMATION:

APPLICANT: Pasternack, Gary R.
TITLE OF INVENTION: No. 5756676e1 Mammalian Protein Associated With
TITLE OF INVENTION: Uncontrolled Cell Division
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner, Birch, McKie & Beckett
STREET: 1001 G Street, N.W.
CITY: Washington, D.C.
STATE: District of Columbia
COUNTRY: U.S.A.
ZIP: 20001

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,066
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER: US 08/314,503
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Posorske Esq., Laurence H.
REGISTRATION NUMBER: 34,698
REFERENCE/DOCKET NUMBER: 1107.47218
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 508-9153
TELEFAX: 202 508-9299
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1052 base pairs
TYPE: nucleic acid

STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE: Homo sapiens
FEATURE: CDS
NAME/KEY: CDS
LOCATION: 97..843
US-08-468-066-1

Query Match 6.6%; Score 40; DB 1; Length 1052;
Best Local Similarity 46.7%; Pred. No. 0.017;
Matches 127; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

QY 59 AGAAGGGAATGTAATCATCATGTTTGAATCTTGAATAACACGCGCTGAAATT 118
DB ACAATAGGAATTTTCAAAATAGTTATTCAGTATCATCTTCTCCCTCATCTTC 820
QY 119 GGTGCTGAATACGAATCATGCTCTGAGTCTTTTCCATTAATTTTCACTACATACC 178
DB 819 AGTTCTGCTTTCCCTTCTGACCCCTTCTTCTTCAACCAAGCTCTTCTCATCTCTC 760
QY 179 CAGTCTCCGACGACGATTAATCAAGCTCCGACATCCCGACCATCCCATTTGAAGTC 238
DB 759 GTCACTTACCTCTCATGTTAATCACTTCTTCACTCTCTCTCTCTCTCTCTCTCT 700
QY 239 AAACACTTAAAGCCTTGCAGAGTCACTGCTTCTTCTTCAACGCGCGCGTGAATGAC 298
DB 699 CTCCTCTTCACT 640
QY 299 CAATTCCT 330
DB 639 TTCATCATCT 608

RESULT 5

US-08-466-717-1/c
Sequence 1, Application US/08466717
Patent No. 5874234

GENERAL INFORMATION:

APPLICANT: Pasternack, Gary R.
TITLE OF INVENTION: No. 5874234e1 Mammalian Protein Associated With
TITLE OF INVENTION: Uncontrolled Cell Division
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner, Birch, McKie & Beckett
STREET: 1001 G Street, N.W.
CITY: Washington, D.C.
STATE: District of Columbia
COUNTRY: U.S.A.
ZIP: 20001

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,717
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER: US 08/314,503
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Posorske Esq., Laurence H.
REGISTRATION NUMBER: 34,698
REFERENCE/DOCKET NUMBER: 1107.47218
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 508-9153
TELEFAX: 202 508-9299
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

LENGTH: 1052 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
ORIGINAL SOURCE: cdna
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 97..843
US-08-466-717-1

Query Match 6.6%; Score 40; DB 2; Length 1052;
Best Local Similarity 46.7%; Pred. No. 0.017;
Matches 127; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

QY 59 AGAAGGGAATGTAACATCATCTTTTGAATCTTGAATAACACGCGCTGAATT 118
DB 879 ACAATAGGAATTTTCAAAATAGGTAATTCACCTAGCATCATCTTCCCTCATCTTC 820
QY 119 GGTGTCGTAATACCAATCATGCTCTGCACTTTTCCACTATTTTCACTACATAC 178
DB 819 AGTTCCTGTTTTCGCTTCTGACCCCTTTTCTTCCACCAAGCTTTTCAATCTTCTC 760
QY 179 CAGTCTCCGACGAGTAATCAAGCTCTCATATCCCCCAACCCATCCCATTCAGTC 238
DB 759 GTCATCTACCTCTCATGCTTAAACCTTTCATCTCTCTCTCTCCATCAGTC 700
QY 239 AAACCTTTAAAGCTTTCGCAAGTCACTGCTTTCTTTCACGCGCGGTGAATGAC 298
DB 639 CTCCTCTTACCTTCT 640
QY 239 CAATTCCT 330
DB 639 TTCATCATCT 608

RESULT 6

US-08-466-743-1/c

Sequence 1, Application US/08466743

Patent No. 6040173

GENERAL INFORMATION:

APPLICANT: Pasternack, Gary R.

APPLICANT: Kuhlaida, Francis P.

TITLE OF INVENTION: No. 6040173el Mammalian Protein Associated With

TITLE OF INVENTION: Uncontrolled Cell Division

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Banner, Birch, McKie & Beckett

STREET: 1001 G Street, N.W.

CITY: Washington, D.C.

STATE: District of Columbia

COUNTRY: U.S.A.

ZIP: 20001

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/466,743

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/314,503

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Posorske Esq., Laurence H.

REGISTRATION NUMBER: 34,698

REFERENCE/DOCKET NUMBER: 1107.47218

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202 508-9153

TELEFAX: 202 508-9299

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1052 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
ORIGINAL SOURCE: cdna
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 97..843
US-08-466-743-1

Query Match 6.6%; Score 40; DB 3; Length 1052;
Best Local Similarity 46.7%; Pred. No. 0.017;
Matches 127; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

QY 59 AGAAGGGAATGTAACATCATGTTTGAATCTTGAATAACACATGCGCTGAATT 118
DB 879 ACAATAGGAATTTTCAAAATAGGTAATTCACCTAGCATCATCTTCCCTCATCTTC 820
QY 119 GGTGTCGTAATACCAATCATGCTCTGCACTTTTCCACTATTTTCACTACATAC 178
DB 819 AGTTCCTGTTTTCGCTTCTGACCCCTTTTCTTCCACCAAGCTTTTCAATCTTCTC 760
QY 179 CAGTCTCCGACGAGTAATCAAGCTCTCATATCCCCCAACCCATCCCATTCAGTC 238
DB 759 GTCATCTACCTCTCATGCTTAAACCTTTCATCTCTCTCTCTCTCTCTCTCTCTCT 700
QY 239 AAACCTTTAAAGCTTTCGCAAGTCACTGCTTTCTTTCACGCGCGGTGAATGAC 298
DB 639 CTCCTCTTACCTTCT 640
QY 239 CAATTCCT 330
DB 639 TTCATCATCT 608

RESULT 7

PCT-US95-12414-1/c

Sequence 1, Application PC/TUS9512414

GENERAL INFORMATION:

APPLICANT: Pasternack, Gary R.

APPLICANT: Kuhlaida, Francis P.

TITLE OF INVENTION: Novel Mammalian Protein Associated With

TITLE OF INVENTION: Uncontrolled Cell Division

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Banner & Allegretti, Ltd.

STREET: 1001 G Street, N.W.

CITY: Washington, D.C.

STATE: District of Columbia

COUNTRY: U.S.A.

ZIP: 20001

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/12414

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/314,503

FILING DATE: 22-SEP-1994

ATTORNEY/AGENT INFORMATION:

NAME: Hoscheit Esq., Dale H.

REGISTRATION NUMBER: 19,090

REFERENCE/DOCKET NUMBER: 1107.51507

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202 508-9153

CURRENT APPLICATION NUMBER: US/09/178,252
CURRENT FILING DATE: 1998-10-23
EARLIER APPLICATION NUMBER: 66/065,215
EARLIER FILING DATE: 1997-11-12
EARLIER APPLICATION NUMBER: 60/076,445
EARLIER FILING DATE: 1998-03-02
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO: 26
LENGTH: 1965
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic B.c. toxin gene
US-09-178-252-26

Query Match
Best Local Similarity 5.9%; Score 36.2; DB 3; Length 1965;
Matches 80; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 176 ACCGAGTCTCCAGACGATTTCAAGCTCTTCACATCCCGCCCAACCCATCCCAATTCA 235
DB 1336 ACCAAGCCCGCAACACCTGCGCCGACGACCTCACACACGAGAGCTCCCGCTGAG 1395
QY 236 GTCAACACTTTAAAGCCTTCGCAAGTCACTGTCTTCTTCCACCGCCGCGTGAAT 295
DB 1396 AACAACTTCAACCTCTCTCCACGACGACCTTCTCGCTTCAACACCAAGGAC 1455
QY 296 GACCAATTCCT 328
DB 1456 GGGCCACCTGCGACGCTGGGGTTCGTCGCCGACC 1488

RESULT 13

US-08-574-959A-8/c
Sequence 8, Application US/08574959A
Patent No. 5962224

GENERAL INFORMATION:
APPLICANT: Jaekyoon Shin, Insil Joung, Ratna K. Vadlamudi
APPLICANT: and Jack L. Strominger
TITLE OF INVENTION: p62 POLYPEPTIDES, RELATED POLYPEPTIDES
TITLE OF INVENTION: AND USES THEREFOR
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/574,959A
FILING DATE: 19-DEC-95
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: DFN-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 3211 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:

NAME/KEY: CDS
LOCATION: 439..3157
US-08-574-959A-8

Query Match
Best Local Similarity 5.8%; Score 35.6; DB 2; Length 3211;
Matches 92; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

QY 150 TCTTTCCACTATTTCACCTACATACCACTCTTCCAGACGATTTCAAGCTCTCA 209
DB 2609 TCT 2550
QY 210 CATCCCCCAACCCATCCCAATCAAGTCAAACTTTAAAGCCTTCGCAAGGTCAC 269
DB 2549 TCTTCT 2490
QY 270 TCTTCTCTTTCACGCGCGCGGAAATGACCAATTCCTCTCTCTCTCTCTCTCTCT 329
DB 2489 TCTTCT 2430
QY 330 TGTGCC 335
DB 2429 TCTTCC 2424

RESULT 14

US-09-357-014-8/c
Sequence 8, Application US/09357014
Patent No. 6291645

GENERAL INFORMATION:

APPLICANT: Jaekyoon Shin, Insil Joung, Ratna K. Vadlamudi

APPLICANT: and Jack L. Strominger

TITLE OF INVENTION: p62 POLYPEPTIDES, RELATED POLYPEPTIDES
AND USES THEREFOR

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD

STREET: 60 State Street, Suite 510

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/357,014

FILING DATE: 19-Jul-1999

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/574,959

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Mandragouras, Amy E.

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: DFN-008

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400

TELEFAX: (617)227-5941

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 3211 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 439..3157

SEQUENCE DESCRIPTION: SEQ ID NO: 8:

US-09-357-014-8

Query Match 5.8%; Score 35.6; DB 3; Length 3211;
Best Local Similarity 49.5%; Pred. No. 0.65;
Matches 92; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

QY 150 TCTTTTCCACTTTTTCACCTCACAATACCCAGCTCTTCCAGACAGATTCAGAGCTCTCA 209
DB 2609 TCT 2550

QY 210 CATCCCCCAACCCATTCCTTCAAGTCAACACATTAAAGCCTTCGCAAGTCACTG 269
DB 2549 TCTTCT 2490

QY 270 TCTTCTCTTCAACCGCGCGCGGTAATGACCAATCTCTCTCTCTCTCTCTCTCTCTCT 329
DB 2489 TCTTCT 2430

QY 330 TGTGCC 335
DB 2429 TCTTCC 2424

RESULT 15

US-08-574-959A-6/c
; Sequence 6, Application US/08574959A
; Patent No. 5962224
; GENERAL INFORMATION:
; APPLICANT: Jaekyoon Shin, Insil Joung, Ratna K. Vadlamudi
; APPLICANT: and Jack L. Strominger
; TITLE OF INVENTION: P62 POLYPEPTIDES, RELATED POLYPEPTIDES
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/574,959A
; FILING DATE: 19-DEC-95
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: DFN-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3901 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 439..3847
US-08-574-959A-6

Query Match 5.8%; Score 35.6; DB 2; Length 3901;
Best Local Similarity 49.5%; Pred. No. 0.71;
Matches 92; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

QY 150 TCTTTTCCACTTTTTCACCTCACAATACCCAGCTCTTCCAGACAGATTCAGAGCTCTCA 209
DB 3299 TCTTCT 3240

QY 210 CATCCCCCAACCCATTCCTTCAAGTCAACACATTAAAGCCTTCGCAAGTCACTG 269
DB 3239 TCTTCT 3180

QY 270 TCTTCTCTTCAACCGCGCGCGGTAATGACCAATCTCTCTCTCTCTCTCTCTCTCTCT 329
DB 3179 TCTTCT 3120

QY 330 TGTGCC 335
DB 3119 TCTTCC 3114

Search completed: January 31, 2004, 01:41:41
Job time : 64 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 31, 2004, 01:33:40 ; Search time 310 Seconds

(without alignments)
7159.790 Million cell updates/sec

Title: US-10-021-323-13

Perfect score: 609
Sequence: 1 gtaatagaatcaacttc.....tgaagcttacaatgaag 609

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 2434939 seqs, 1822278265 residues

Total number of hits satisfying chosen parameters: 4869878

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_NA.*
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17: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	82.4	13.5	279	10	US-09-878-574-5466 Sequence 5466, App
2	81.2	13.3	381	9	US-09-770-791-166 Sequence 166, App
3	78.6	12.9	244	10	US-09-878-574-10284 Sequence 10284, A
4	55.6	9.1	576	10	US-09-938-842A-2017 Sequence 2017, A
5	55.6	9.1	576	12	US-09-938-842A-2017 Sequence 1697, App
6	53.6	8.8	510	10	US-09-938-842A-1697 Sequence 1697, App
7	53.6	8.8	510	12	US-09-938-842A-1697 Sequence 1697, App
8	43.8	7.2	644	12	US-10-341-961A-130 Sequence 130, App
9	43	7.1	905	16	US-10-273-334-7 Sequence 7, Appli
10	43	7.1	905	16	US-10-273-334-19 Sequence 19, Appli
11	43	7.1	905	16	US-10-273-334-26 Sequence 26, Appli
12	43	7.1	907	16	US-10-273-334-4 Sequence 4, Appli
13	41.6	6.8	907	16	US-10-273-334-30 Sequence 30, Appli
14	41.6	6.8	5928	13	US-10-311-455-2211 Sequence 2211, App
15	40.8	6.7	456	12	US-10-260-238-771 Sequence 771, App

16	40.8	6.7	671	15	US-10-184-644-346 Sequence 346, App
17	40.8	6.7	671	15	US-10-184-634-346 Sequence 346, App
18	40.4	6.6	520	15	US-10-184-644-332 Sequence 332, App
19	40.4	6.6	520	15	US-10-184-634-332 Sequence 332, App
20	40	6.6	905	16	US-10-273-334-11 Sequence 11, Appli
21	40	6.6	905	16	US-10-273-334-17 Sequence 17, Appli
22	40	6.6	907	16	US-10-273-334-9 Sequence 9, Appli
23	40	6.6	907	16	US-10-273-334-13 Sequence 13, Appli
24	40	6.6	907	16	US-10-273-334-25 Sequence 25, Appli
25	40	6.6	907	16	US-10-273-334-28 Sequence 28, Appli
26	40	6.6	908	16	US-10-273-334-32 Sequence 32, Appli
27	39.6	6.5	423	10	US-09-938-842A-592 Sequence 592, App
28	39.6	6.5	423	12	US-09-938-842A-592 Sequence 592, App
29	38.6	6.4	7183	15	US-10-198-846-11576 Sequence 11576, A
30	38.6	6.3	821	13	US-10-027-632-154321 Sequence 154321, Sequence 382, App
31	38.6	6.3	821	14	US-10-027-632-154321 Sequence 382, App
32	38.4	6.3	889	16	US-10-273-334-3 Sequence 3, Appli
33	38.4	6.3	889	16	US-10-273-334-15 Sequence 15, Appli
34	38.4	6.3	895	16	US-10-273-334-21 Sequence 21, Appli
35	38.4	6.3	895	16	US-10-273-334-6 Sequence 6, Appli
36	38.4	6.3	907	16	US-10-273-334-1 Sequence 1, Appli
37	38.4	6.3	5785	16	US-10-240-452-24 Sequence 24, Appli
38	38	6.2	7231	13	US-10-213-700-2 Sequence 2, Appli
39	37.8	6.2	966	15	US-10-439-388-4 Sequence 4, Appli
40	37.8	6.2	1475	12	US-10-085-117-334 Sequence 334, App
41	37.8	6.2	154817	13	US-10-027-632-179264 Sequence 179264, Sequence 179264, Sequence 10, Appli
42	37.8	6.2	1223197	13	US-10-027-632-179264 Sequence 10, Appli
43	37.8	6.2	1223197	14	US-10-027-632-179264 Sequence 10, Appli
44	37.6	6.2	594	13	US-10-140-472-10 Sequence 10, Appli
45	37.6	6.2	594	13	US-10-141-761-10 Sequence 10, Appli

ALIGNMENTS

RESULT 1
US-09-878-574-5466/c
; Sequence 5466, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plates
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 5466
; LENGTH: 279
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 701097008H1
US-09-878-574-5466

Query Match	13.5%	Score 82.4;	DB 10;	Length 279;
Best Local Similarity	62.5%	Pred. No. 2.2e-15;		
Matches 145;	Conservative	0;	Mismatches 86;	Indels 1;
			Gaps 1;	
QY	345	GAGATGGATTCCTAAGAGCAAGATTCATCCAGTTCATCAAGTTCCTCCACTAG	404	
DB	279	GATATGGATTCCTAAGAGCAAGATTCATCCAGTTCATCAAGTTCCTCCACTAG	221	
QY	405	GGCTCCATTCCTCCAGGCTGATTCAGACAGCCGATTCCTCCAGGACCAATTCAGC	464	
DB	220	GATTCACATTCCTCCAGGCTGATTCAGACAGCCGATTCCTCCAGGACCAATTCAGC	161	
QY	465	TCTTCAGACTACAGACCATTCCTTCCTGAGCTTCGAAATACGCTTCGAG	524	
DB	160	TCTTCAGACTACAGACCATTCCTTCCTGAGCTTCGAAATACGCTTCGAG	101	

QY 525 TCGTCTTACTAAGGGGAGCATTTTACCAACCAAGAGATATGATCCCAT 576
DB 100 TCAGTTGGTGTGTAGAGACACATTTTGGGTATTAACATGATTTAAAGCCT 49

RESULT 2

US-09-770-791-166
Sequence 166, Application US/09770791
Patent No. US20020062014A1

GENERAL INFORMATION:

APPLICANT: Goriach, Jörn
APPLICANT: An, Yong-Qiang
APPLICANT: Hamilton, Carol M.
APPLICANT: Price, Jennifer L.
APPLICANT: Raines, Tracy M.
APPLICANT: Yu, Yang
APPLICANT: Rameaka, Joshua G.
APPLICANT: Page, Amy
APPLICANT: Matthew, Abraham V.
APPLICANT: Ledford, Brooke L.
APPLICANT: Moesner, Jeffrey P.
APPLICANT: Haas, William David
APPLICANT: Garcia, Carlos A.
APPLICANT: Krickler, Maja
APPLICANT: Slader, Ted
APPLICANT: Davis, Keith R.
APPLICANT: Allen, Keith
APPLICANT: Hoffman, Neil
APPLICANT: Hufman, Patrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
FILE REFERENCE: 2029 (PABA-018PRV)
CURRENT FILING DATE: 2001-01-26
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 166
LENGTH: 381
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-770-791-166

Query Match 13.3%; Score 81.2; DB 9; Length 381;
Best Local Similarity 61.2%; Pred. No. 6; Se-15;
Matches 131; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

QY 68 ATGTAAATCATGTTTGAATTTGAAATCAACATGCGCTGAATTGGTGTGTA 127
DB 167 ATGTAAATCATGTTTGAATTTGAAATCAACATGCGCTGAATTGGTGTGTA 226
QY 128 ATACCAATCATGCTCTGAGCTCTTTCCACTATTTTCACTCAATACCAAGTCTTC 187
DB 227 AACTGGAATCATTTCCCAATCCCAAGCCTTTGCTCTCTCAAAACCTAGCCGTTTC 286
QY 188 CAGCAGATTTAAAGTCTCTCATATCCCCCAACCAATCCATTCAGTCAAAAGCTTT 247
DB 287 CAACACATCATCAAGACTCTCTCGCTGAATATATACATCTCCGTTCATCATGACACAT 346
QY 248 AAAAGCTTGGCAAGTCACTGTCTTCTTCTCA 281
DB 347 AAAGCCTTGGCAATGCTTCAATCATATACGCA 380

RESULT 3

US-09-878-574-10284/C
Sequence 10284, Application US/09878574
Patent No. US20020110348A1
GENERAL INFORMATION:
APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.

APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-2115401B
CURRENT FILING DATE: 2001-12-21
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO: 10284
LENGTH: 244
TYPE: DNA
ORGANISM: Glycine max
OTHER INFORMATION: Clone ID: 701103505H1
US-09-878-574-10284

Query Match 12.9%; Score 78.6; DB 10; Length 244;
Best Local Similarity 60.6%; Pred. No. 3; Se-14;
Matches 129; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 364 ACAAGATTCATCCAGTTCAACATGTTTCCCAAGGCTCCCAATTTCAAGGC 423
DB 244 ACAAGATTCATCCAGTTCAACATGTTTCCCAAGGCTCCCAATTTCAAGGC 185
QY 424 TGAATGGACAGACCCGATTTCTGAGCAACCAATTCAGCTCCCAAGCAAGC 483
DB 184 TATATGGGAATTCGCGTCACTGAGCAATGATTCAGTTCTCAAGGCTCAATC 125
QY 484 CATTCATTTCTTGTGAGCTTCTGCAATACGCTTGAAGTCCGCTTACTAAGGGGG 543
DB 124 CGTGCATTCACGCTCCCACTTTCTCAAAATACGCTTCAAGGCAAGTCTGTAGAGAC 65
QY 544 ACATTTTACCAACCAAGGATATGATCAACAT 576
DB 64 AGTATTTGCAATTAAGGCAATTTAAAGCCT 32

RESULT 4

US-09-938-842A-2017/C
Sequence 2017, Application US/09938842A
Patent No. US20020160378A1

GENERAL INFORMATION:

APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Zhang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
FILE REFERENCE: S001300-3
CURRENT FILING DATE: 2001-08-24
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO: 2017
LENGTH: 576
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-938-842A-2017

Query Match 9.1%; Score 55.6; DB 10; Length 576;
Best Local Similarity 49.7%; Pred. No. 1e-06;
Matches 170; Conservative 0; Mismatches 169; Indels 3; Gaps 1;

QY 74 CATATGTTTGAATTTGAAATCAACATGCGCTGAAATGATGCTGATATACCA 133
DB 549 CATATGTTTGAATTTGAAATCAACATGCGCTGAAATGATGCTGATATACCA 490
QY 134 AATCATGCTCTGAGTCTTTTCACTATTTTCACTACATACCAAGTCTTCCAGAC 193

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Db      489 GATCATCTTCTCACTCTCTCCATTTCTCCACCTTCAAGGTAACCAAGTTTCTTCAGAAC 430
Qy      194 GATTCAGAGCTCTCATACCCCAACCCATCCCATTCAGTCAAAACATTAAAGC 253
Db      429 AGTTTGCAAGTTCTTAGCGGAGATGATCATCACCGTTCTCATCAACCTTAAACGC 370
Qy      254 CTTCGCAAGGTCACTGTCTTCTTCTTCACCGCGCCGCGTGAATGACCAATTCTCTCTCTC 313
Db      369 CTTCGCGAGATC---CGATTCAATTTTCACTCTGCGAAGAAAGATCATCTTCTCTCTCC 313
Qy      314 CTCTTGTCACCAACCATGTGTCAGAGGGTTCAGATGATTCATTAAGAACAGAAATTC 373
Db      312 TCCTCCACAGCTCCACCGAAGAAATGTCAGTGTGTTGTGAAGAGAAAGAAATC 253
Qy      374 ATCCAGTTCAAAACATGTTTCCCACTAAGGCTCCCAATTC 415
Db      252 ATCGAAATTGAGACCAAGTGTTCACAGTTGATGTATTC 211
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RESULT 5

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US-09-938-842A-2017/c
; Sequence 2017, Application US/09938842A
; Publication No. US20040009476A9
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 2017
; LENGTH: 576
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2017
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Query Match      9.1%; Score 55.6; DB 12; Length 576;
Best Local Similarity 49.7%; Pred. No. 1e-06;
Matches 170; Conservative 0; Mismatches 169; Indels 3; Gaps 1;
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Qy      74 CATCATGTTTGAATTTGAAATCAACATCCGCTGTAATGGTGTCTGTAATACCA 133
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Qy      134 AATCATGCTCCGCACTCTTTCATATTTCACTCACTCACTCACTCACTCACTCACTCA 193
Db      489 GATCATCTTCTCACTCTCTCCATTTCTCACTTGAAGTAAACCAAGTTTCTTCAGAAC 430
Qy      194 GATTCAGAGCTCTCATACCCCAACCCATCCCATTCAGTCAAAACATTAAAGC 253
Db      429 AGTTTGCAAGTTCTTAGCGGAGATGATCATCACCGTTCTCATCAACCTTAAACGC 370
Qy      254 CTTCGCAAGGTCACTGTCTTCTTCTTCACCGCGCCGCGTGAATGACCAATTCTCTCTCTC 313
Db      369 CTTCGCGAGATC---CGATTCAATTTTCACTCTGCGAAGAAAGATCATCTTCTCTCTCC 313
Qy      314 CTCTTGTCACCAACCATGTGTCAGAGGGTTCAGATGATTCATTAAGAACAGAAATTC 373
Db      312 TCCTCCACAGCTCCACCGAAGAAATGTCAGTGTGTTGTGAAGAGAAAGAAATC 253
Qy      374 ATCCAGTTCAAAACATGTTTCCCACTAAGGCTCCCAATTC 415
Db      252 ATCGAAATTGAGACCAAGTGTTCACAGTTGATGTATTC 211
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Db      252 ATCGAAATTGAGACCAAGTGTTCACAGTTGATGTATTC 211
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RESULT 6

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US-09-938-842A-1697/c
; Sequence 1697, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1697
; LENGTH: 510
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1697
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Query Match      8.8%; Score 53.6; DB 10; Length 510;
Best Local Similarity 52.7%; Pred. No. 4e-06;
Matches 116; Conservative 0; Mismatches 104; Indels 0; Gaps 0;
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Qy      74 CATCATGTTTGAATTTGAAATCAACATCCGCTGTAATGGTGTCTGTAATACCA 133
Db      480 CATCATGTAAGAAACTCTTGTATGATGATCATCATCACCATCTGCATCAACTTGAT 421
Qy      134 AATCATGCTCCGCACTCTTTCATATTTCACTCACTCACTCACTCACTCACTCACTCA 193
Db      420 AATCATCTTCTTACCAACATCTAGGGTCTTCCTGCTGAGTCCCAAGAACCATAC 361
Qy      194 GATTCAGAGCTCTCATACCCCAACCCATCCCATTCAGTCAAAACATTAAAGC 253
Db      360 AGATTTCAGCTCTTCAGAGATGATTAACCATCTCCGCTTGCTCAACAGCTTAAAGC 301
Qy      254 CTTCGCAAGGTCACTGTCTTCTTCTTCACCGCGCCGCTGA 293
Db      300 ATCTTCATATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 261
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RESULT 7

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US-09-938-842A-1697/c
; Sequence 1697, Application US/09938842A
; Publication No. US20040009476A9
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1697
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LENGTH: 510
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-938-842A-1697

Query Match 8.8%; Score 53.6; DB 12; Length 510;

Best Local Similarity 52.7%; Pred. No. 4e-06; Mismatches 104; Indels 0; Gaps 0;

Matches 116; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

QY 74 CATCATGTTTGAATTTCTTGAATCAACCATGCCGTGTAATGTTGTAATACCA 133
DB 480 CATCATGTTTGAATTTCTTGAATCAACCATGCCGTGTAATGTTGTAATACCA 421
QY 134 AATCATGCTCTGCAAGTCTTTTCACTATTTTCACTCATACCATCCAGCTTCCAGAC 193
DB 420 AATCATGCTCTTCAACCATCTAGAGGTCTTCCCTGCTGTAAGTCCAGAAAGCATCAG 361
QY 194 GATTCAGCTCTGCAAGTCTTTTCACTATTTTCACTCATACCATCCAGCTTCCAGAC 253
DB 360 AATTCAGCTCTTCAACCATCTAGAGGTCTTCCCTGCTGTAAGTCCAGAAAGCATCAG 301
QY 254 CTTCGCAAGTCACTGTCTTCTTCTTCAACCGCCGCGTGA 293
DB 300 ATCTTCATATCTCTTCTCTGTTGCGCATCGTTGTA 261

RESULT 8

US-10-341-961A-130/c
Sequence 130, Application US/10341961A
Publication No. US20040006787A1

GENERAL INFORMATION:

APPLICANT: Boyce Thompson Institute for Plant Research, Inc.

APPLICANT: Chugan Corporation

APPLICANT: Crasica, Oswald

APPLICANT: Swirsky, Peter

APPLICANT: Mysore, Kiran

APPLICANT: Folkerts, Otto

APPLICANT: Martin, Gregory

APPLICANT: Ekengren, Sophia

TITLE OF INVENTION: PLANT DEFENSE-RELATED GENES REGULATED IN RESPONSE TO PLANT-PATHOGE

FILE REFERENCE: BTI.67A2

CURRENT FILING DATE: 2003-01-14

PRIOR APPLICATION NUMBER: 60390249

PRIOR FILING DATE: 2002-06-20

PRIOR APPLICATION NUMBER: 60261029

PRIOR FILING DATE: 2001-01-11

PRIOR APPLICATION NUMBER: 60348792

PRIOR FILING DATE: 2002-01-14

NUMBER OF SEQ ID NOS: 395

SOFTWARE: PatentIn version 3.1

SEQ ID NO 130

LENGTH: 644

TYPE: DNA

ORGANISM: Lycopersicon esculentum

US-10-341-961A-130

Query Match 7.2%; Score 43.8; DB 12; Length 644;

Best Local Similarity 50.7%; Pred. No. 0.0058; Mismatches 105; Conservative 0; Mismatches 102; Indels 0; Gaps 0;

QY 74 CATCATGTTTGAATTTCTTGAATCAACCATGCCGTGTAATGTTGTAATACCA 133
DB 638 CATCATGTTTGAATTTCTTGAATCAACCATGCCGTGTAATGTTGTAATACCA 579
QY 134 AATCATGCTCTGCAAGTCTTTTCACTATTTTCACTCATACCATCCAGCTTCCAGAC 193
DB 578 AATCATGCTCTTCAACCATCTAGAGGTCTTCCCTGCTGTAAGTCCAGAAAGCATCAG 519
QY 194 GATTCAGCTCTGCAAGTCTTTTCACTATTTTCACTCATACCATCCAGCTTCCAGAC 253
DB 518 CACGCAATTCCTTCTGCGCATATTAATTCATCCCGTTCCTGTAATAAATCAAGC 459

QY 254 CTTCGCAAGTCACTGTCTTCTCTTC 280
DB 458 TTCTTCGATCATTCATTCCTGTGC 432

RESULT 9

US-10-273-334-7/c

Sequence 7, Application US/10273334

Publication No. US20030129631A1

GENERAL INFORMATION:

APPLICANT: Pasteurack, Gary R.

APPLICANT: Kochevav, Gerald J.

APPLICANT: Brody, Jonathan R.

APPLICANT: Kodkol, Shihari S.

TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY

FILE REFERENCE: 031787.0076

CURRENT FILING DATE: 2002-10-18

PRIOR APPLICATION NUMBER: US/09/591,500

PRIOR FILING DATE: 2000-12-06

PRIOR APPLICATION NUMBER: PCT/US98/26433

PRIOR FILING DATE: 1998-12-11

PRIOR APPLICATION NUMBER: US 60/069,677

PRIOR FILING DATE: 1997-12-11

NUMBER OF SEQ ID NOS: 51

SOFTWARE: PatentIn version 3.1

SEQ ID NO 7

LENGTH: 905

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (64)..(453)

OTHER INFORMATION:

US-10-273-334-7

Query Match 7.1%; Score 43; DB 16; Length 905;

Best Local Similarity 47.0%; Pred. No. 0.013; Mismatches 133; Conservative 0; Mismatches 130; Indels 0; Gaps 0;

QY 48 AGAATACTCAAGACGGAATGTACATCATGTTTGAATTTGTAATCAACCATG 107
DB 857 ACAGTAATAATCAAGAAATTTTCAAAATATATATTCATTCAGGATCGCTTCT 798
QY 108 CCGTGAATGTTGTTGTAATACCAATATGCTCTGCAAGTCTTTTCACTATTTC 167
DB 797 CCGTGAATGTTGTTGTAATACCAATATGCTCTGCAAGTCTTTTCACTATTTC 738
QY 168 CCGTGAATGTTGTTGTAATACCAATATGCTCTGCAAGTCTTTTCACTATTTC 227
DB 737 TCATCTCTCATATATCATCTCTCCATTTGTAATACCTTCATCTCTCTCTCT 678
QY 228 CCATTCAGTCAACACTTTAAAGCTTCGCAAGTCACTGTCTTTTCAACGCGG 287
DB 677 CCATTCAGTCTCTCTCTTCAAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 618
QY 288 CCGTGAATGACCAATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 330
DB 617 ACCTGACATTCATCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 575

RESULT 10

US-10-273-334-19/c

Sequence 19, Application US/10273334

Publication No. US20030129631A1

GENERAL INFORMATION:

APPLICANT: Pasteurack, Gary R.

APPLICANT: Kochevav, Gerald J.

APPLICANT: Brody, Jonathan R.

APPLICANT: Kodkol, Shihari S.

TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY

FILE REFERENCE: 031787.0076

;; CURRENT APPLICATION NUMBER: US/10/273,334
;; CURRENT FILING DATE: 2002-10-18
;; PRIOR APPLICATION NUMBER: US/09/591,500
;; PRIOR FILING DATE: 2000-12-06
;; PRIOR APPLICATION NUMBER: PCT/US98/26433
;; PRIOR FILING DATE: 1998-12-11
;; PRIOR APPLICATION NUMBER: US 60/069,677
;; PRIOR FILING DATE: 1997-12-11
;; NUMBER OF SEQ ID NOS: 51
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 19
;; LENGTH: 905
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (64)..(453)
;; OTHER INFORMATION:
US-10-273-334-19

Query Match 7.1%; Score 43; DB 16; Length 905;
Best Local Similarity 47.0%; Pred. No. 0.013;
Matches 133; Conservative 0; Mismatches 150; Indels 0; Gaps 0;

QY 48 AGAATAACTCAAGAAAGGGAATGTAAACATCATGTTTGAATTTGAAATCAACCATG 107
DB 857 ACAGTAAATCAAAAAGAAATTTTCAAAATAGATTATTCACACTAGGACATGCTTCT 798
QY 108 CCGTCTGAATGGTGTCTGTAATACCAATCATGCTCTGACGTCTTTTCCACTATTTTCA 167
DB 797 CCTCATCTTCAGTTCTTATTTTGGCTTCTGACCCCTTTCTTCCACCAAGCTCTTCT 738
QY 168 CCTCATACCCAGTCTTCCAGCAGATTCAGAGTCTCTCATACCCCAACCATCC 227
DB 737 TCATCTTCTCATCATCACTTCCATCTCATTTGTAATACCTTCTCTCTCTCTCT 678
QY 228 CCATTCAGTCAAAACATTAAAGCCTTCGCAAGGTCTCTCTTCTTCCACGCGCG 287
DB 677 CCATCAGTCTCTCTCTTCAAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 618
QY 288 CCGTGAATGACCAATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 330
DB 617 ACCTGAGCATCTTCAATCATCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 575

RESULT 11
US-10-273-334-26/c
;; Sequence 26, Application US/10273334
;; Publication No. US20030129631A1
;; GENERAL INFORMATION:
;; APPLICANT: Pasternack, Gary R.
;; APPLICANT: Kochneva, Gerald J.
;; APPLICANT: Brody, Jonathan R.
;; APPLICANT: Kodkol, Shrihari S.
;; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
;; FILE REFERENCE: 031787.0076
;; CURRENT APPLICATION NUMBER: US/10/273,334
;; CURRENT FILING DATE: 2002-10-18
;; PRIOR APPLICATION NUMBER: US/09/591,500
;; PRIOR FILING DATE: 2000-12-06
;; PRIOR APPLICATION NUMBER: PCT/US98/26433
;; PRIOR FILING DATE: 1998-12-11
;; PRIOR APPLICATION NUMBER: US 60/069,677
;; PRIOR FILING DATE: 1997-12-11
;; NUMBER OF SEQ ID NOS: 51
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 26
;; LENGTH: 905
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (64)..(453)

;; OTHER INFORMATION:
US-10-273-334-26

Query Match 7.1%; Score 43; DB 16; Length 905;
Best Local Similarity 47.0%; Pred. No. 0.013;
Matches 133; Conservative 0; Mismatches 150; Indels 0; Gaps 0;

QY 48 AGAATAACTCAAGAAAGGGAATGTAAACATCATGTTTGAATTTGAAATCAACCATG 107
DB 857 ACAGTAAATCAAAAAGAAATTTTCAAAATAGATTATTCACACTAGGACATGCTTCT 798
QY 108 CCGTCTGAATGGTGTCTGTAATACCAATCATGCTCTGACGTCTTTTCCACTATTTTCA 167
DB 797 CCTCATCTTCAGTTCTTATTTTGGCTTCTGACCCCTTTCTTCCACCAAGCTCTTCT 738
QY 168 CCTCATACCCAGTCTTCCAGCAGATTCAGAGTCTCTCATACCCCAACCATCC 227
DB 737 TCATCTTCTCATCATCACTTCCATCTCATTTGTAATACCTTCTCTCTCTCTCT 678
QY 228 CCATTCAGTCAAAACATTAAAGCCTTCGCAAGGTCTCTCTTCTTCCACGCGCG 287
DB 677 CCATCAGTCTCTCTCTTCAAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 618
QY 288 CCGTGAATGACCAATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 330
DB 617 ACCTGAGCATCTTCAATCATCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 575

RESULT 12
US-10-273-334-4/c
;; Sequence 4, Application US/10273334
;; Publication No. US20030129631A1
;; GENERAL INFORMATION:
;; APPLICANT: Pasternack, Gary R.
;; APPLICANT: Kochneva, Gerald J.
;; APPLICANT: Brody, Jonathan R.
;; APPLICANT: Kodkol, Shrihari S.
;; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
;; FILE REFERENCE: 031787.0076
;; CURRENT APPLICATION NUMBER: US/10/273,334
;; CURRENT FILING DATE: 2002-10-18
;; PRIOR APPLICATION NUMBER: US/09/591,500
;; PRIOR FILING DATE: 2000-12-06
;; PRIOR APPLICATION NUMBER: PCT/US98/26433
;; PRIOR FILING DATE: 1998-12-11
;; PRIOR APPLICATION NUMBER: US 60/069,677
;; PRIOR FILING DATE: 1997-12-11
;; NUMBER OF SEQ ID NOS: 51
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 4
;; LENGTH: 907
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-273-334-4

Query Match 7.1%; Score 43; DB 16; Length 907;
Best Local Similarity 47.0%; Pred. No. 0.013;
Matches 133; Conservative 0; Mismatches 150; Indels 0; Gaps 0;

QY 48 AGAATAACTCAAGAAAGGGAATGTAAACATCATGTTTGAATTTGAAATCAACCATG 107
DB 859 ACAGTAAATCAAAAAGAAATTTTCAAAATAGATTATTCACACTAGGACATGCTTCT 800
QY 108 CCGTCTGAATGGTGTCTGTAATACCAATCATGCTCTGACGTCTTTTCCACTATTTTCA 167
DB 799 CCTCATCTTCAGTTCTTATTTTGGCTTCTGACCCCTTTCTTCCACCAAGCTCTTCT 740
QY 168 CCTCATACCCAGTCTTCCAGCAGATTCAGAGTCTCTCATACCCCAACCATCC 227
DB 739 TCATCTTCTCATCATCACTTCCATCTCATTTGTAATACCTTCTCTCTCTCTCT 680
QY 228 CCATTCAGTCAAAACATTAAAGCCTTCGCAAGGTCTCTCTTCTTCCACGCGCG 287

LOCATION: (382) (382)

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; OTHER INFORMATION: n = any nucleotide
; FEATURE:
; NAME/KEY: N_region
; LOCATION: (385)..(385)
; OTHER INFORMATION: n = any nucleotide
; FEATURE:
; NAME/KEY: N_region
; LOCATION: (409)..(409)
; OTHER INFORMATION: n = any nucleotide
; FEATURE:
; NAME/KEY: N_region
; LOCATION: (423)..(423)
; OTHER INFORMATION: n = any nucleotide
; FEATURE:
; NAME/KEY: N_region
; LOCATION: (436)..(436)
; OTHER INFORMATION: n = any nucleotide
US-10-260-238-771

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Query Match 6.7%; Score 40.8; DB 12; Length 456;
Best Local Similarity 48.6%; Pred. No. 0.041;
Matches 102; Conservative 0; Mismatches 108; Indels 0; Gaps 0;

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QY 107 GCCGCTGATTGGTGTGTAATACCAATCATGCTTCGAGTCTTTTCACCTATTTC 166
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DB 453 GCCGTTGCCGTGCGGCTNCACATGCTGATNATTCGCGGCGAGTNGTCGCGGCGGCC 394
    |||||

QY 167 ACCTACATATCCAGTCTTCCGACAGTATTCAGTCTCTCATATCCCCCAACCATC 226
    |||||
DB 393 ATGCTTGANCCNGAGGCTGAGACAGGACCGGAGCTNGTGCACGGTATGATGATCCGTC 334
    |||||

QY 227 CCATTCAGTCAACACTTTAAAGCCTTCGCAAGTCACTGTCTTCTTCTTCACCGCC 286
    |||||
DB 333 GCCGTTCTGTGTCGACAGTGAACGCTCCCGGATCCCTCTCTGTCGTGCGGGGC 274
    |||||

QY 287 GCCGTAATGACCAATTCTCTCTCTC 316
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DB 273 GCCGCCCTTGCCGCCGATGCGCCGCCGCCG 244
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Search completed: January 31, 2004, 02:37:42
Job time : 317 secs

